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GenCore version 5.1.4_p5_4578
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- protein search, using sw model OM protein 8, 2003, 16:41:13; search time 22 Seconds Мау Run on:

(without alignments)
2119.327 Million cell updates/sec

US-09-926-163B-2

1 MITRETLKSLPANVQAPPYD.......KVIVLRKIIREKGVKAAIPA 485 Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

0

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

					SUMMARIES	
		#P				
Result		Query				
NO.	Score	Match	Length	BB	QI	Description
Т	13	2.7	464	7	AG3103	mannitol 2-dehydro
2	13	2.7	525	~	C98183	
m	10	2.1	486	7	S56548	fructuronate reduc
4	10	2.1	486	7	B91289	D-mannonate oxidor
ū	10	2.1	486	7	E86130	mannonate oxidored
9	10	2.1	491	7	D83353	mannitol dehydroge
7	6	1.9	486	7	A64909	probable fructuron
ထ	6	1.9	486	7	690897	probable oxidoredu
5	σ	1.9	486	7	H85719	probable oxidoredu
10	6	1.9	488	7	AD0679	fructuronate reduc
11	80	1.6	244	~	B97627	hypothetical prote
12	80	1.6	244	~	AD2850 .	
13	80	1.6	253	7	S76761	hypothetical prote
14	œ	1.6	260	7	140886	0
15	80	1.6	384	~	S73429	glycerol-3-phospat
16	80	1.6	409	~	T36940	probable oxidoredu
17	80	1.6	463		AF0283	probable mannitol
18	8	1.6	580		A86834	1-deoxyxylulose-5-
19	7	1.4	42.		T13269	hypothetical prote
20	7	1.4			н81016	hypothetical prote
21	7	1.4	77		A47070	ferrochelatase (EC
22	7	1.4		7	AI1875	hypothetical prote
23	7	1.4		~	S77423	
24	7	1.4	142	~	C87255	transcription regu
25	7	1.4		7	A90524	hypothetical prote
56	7	1.4		7	B69840	conserved hypothet
27	7	1.4	16	7	D83953	hypothetical prote
28	7	1.4	171	7	12	conserved hypothet
29	. 7	1.4	172	7	T45196	probable transcrip

MG428 homolog C12_	hypothetical prote	probable transfera	probable transfera	hypothetical prote	DNA-directed RNA p	peptidyl-prolyl ci	urease accessory p	glutathione transf	ribosomal protein	hypothetical prote	colanic acid biosy	regulator of capsu	hypothetical prote	colanic acid biosy	hypothetical prote
S73542	F69936	286062	F85831	E64971	S20586	G87370	AD1898	XUFF11	A48226	A87446	BVECCB	AC0790	D85861	B91017	A82190
7	7	7	~	7	7	7	7	7	7	7	-	~	7	N	7
172	179	182	182	182	203	205	206	209	210	214	216	216	216	216	221
1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4
7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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E	~
5	C
S	5

RESULT 1
AG3103
manniol 2-dehydrogenase mtlK [imported] - Agrobacterium tumefaciens (strain C58, Dup c. Species: Agrobacterium tumefaciens
C. Species: Agrobacterium tumefaciens
C. Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002.
C. Accession: AG3103
R. F. Wood, D. W.; Setubal, J. C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McC1; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2333, 2001
A. Alauthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:11743193

A;Accession: AG3103

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-494 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45245.1; PID:g17742929; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:

A; Gene: mtlK

A;Map position: linear chromosome C;Superfamily: conserved hypothetical protein YEL070w

Gaps ö Length 494; Indels Ouery Match 2.7%; Score 13; DB 2; Le Best Local Similarity 100.0%; Pred. No. 8.3e-05; Matches 13; Conservative 0; Mismatches 0;

; 0

123 IRIVSMTITEGGY 135 ò

124 IRIVSMTITEGGY 136 g

RESULT 2 C98183

mannitol 2-dehydrogenase (mdh) [imported] - Agrobacterium tumefaciens (strain C58, Ce C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11.Jan-2002
C; Accession: C9818
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm A; Edu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 201
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Accession: C98183
A; Status: preliminary

A;MOlecule rype: DNA A;Residues: 1-525 <KUR> A;Cross-references: GB:AE007870; PIDN:AAX88989.1; PID:g15158773; GSPDB:GN00170 C;Genetics:

A; Gene: AGR_L_830

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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: B86130
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-491 <STO>
A;Cross-references: GB:AE004660; GB:AE004091; NID:g9948372; PIDN:AAG05730.1; GSPDB:GN
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A)Residues: 11486 <STO>
A)Cross-references: GB:AE005174; NID:g12519333; PIDN:AAG59505.1; GSPDB:GN00145; UWGP:
A)Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mannonate oxidoreductase [imported] - Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mannitol dehydrogenase PA2342 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                       A;Cross-references: GB:BA000007; PIDN:BAB38705.1; PID:g13364760; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: E86130
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C;Superfamily: conserved hypothetical protein YEL070w
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A;Gene: mtlD; PA2342
C;Superfamily: conserved hypothetical protein YEL070w
                                                                                   C;Genetics:
A;Gene: ECS5282
C;Superfamily: conserved hypothetical protein YEL070w
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0.11;
                                                                                                                                                                                                 2.1%; Score 10; DB 2;
100.0%; Pred. No. 0.11;
tive 0; Mismatches
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100.0%; Pred. No. 0.11;
ative 0; Mismatches
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100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                                    Query Match 2.1
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                         181 KAFTVMSCDN 190
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                                                                                                                                                                                                                                                                                                                                                   178 KAFTVMSCDN 187
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 10; Conserv
  A; Residues: 1-486 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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A; Residues: 17486 <BUR>
A; Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97219.1; PID:g537164
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
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C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C; Accession: B91289

R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res, 8, 11-22, 2001

A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc

A; Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Date: 28-Oct-1995 #sequence_revision 13-Mar-1997 #text_change 01-Mar-2002
C,Accession: SS6548; B65246
R;Burland, V,; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A;Reference number: S56314; MUID:95334362; PMID:7610040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-486 <BLAT>
A;Cross-references: GB:AE000503; GB:U00096; NID:g1790777; PIDN:AAC77279.1; PID:g1790779;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: uxuB
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Description: reversible reaction of D-mannonate and NAD(+) to D-fructuronate and NADH A, Pathway: D-glucuronate catabolism A, Pathway: D-glucuronate catabolism A, Note: part of the interconversion of D-fructuronate to D-2-keto-3-deoxy-D-gluconate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D-mannonate oxidoreductase ECs5282 [imported] - Escherichia coli (strain 0157:H7, subst)
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                                                                                                                                                                                                                                                                                                                                                                                                            - Escherichia coli (strain K-12)
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C;Superfamily: conserved hypothetical protein YEL070w
C;Keywords: carbon-oxygen lyase; hydro-lyase; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                         Length 525;
                                                                                                                                                  Indels
                                                                                      2.7%; Score 13; DB 2; L6
100.0%; Pred. No. 8.8e-05;
tive 0; Mismatches 0;
A;Map position: linear chromosome
C;Superfamily: conserved hypothetical protein YEL070w
                                                                                                                                                                                                                                                                                                                                                                                                         fructuronate reductase (EC 1.1.1.57) uxuB - Es
N;Alternate names: D-mannonate oxidoreductase
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                  Conservative
                                                                                                                                                                                                       IRIVSMTITEGGY 135
                                                                                                                                                                                                                                        155 IRIVSMTITEGGY 167
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                                                                                                                 Local Similarity
nes 13; Conserv
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Best Local S
Matches 13
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THE PERSON NAMED IN

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fructuronate reductase (EC 1.1.1.57) - Salmonella enterica subsp. enterica serovar Ty
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: AD0679

R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moule, S.; O'Gaora, P.

Nature 413, 848 8852, 2001

A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A; Reference number: AB0502; PMID:11677608

A; Scatus; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Accession: B97627
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Reference number: A97359; PMID:11743194
                                                                                                   probable oxidoreductase ydfI [imported] - Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-486 <STO>
A;Cross-references: GB:AE005174; NID:g12515111; PIDN:AAG56220.1; GSPDB:GN00145; UWGP:A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C58,
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                                          C.Species: Escherichia coli
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                           A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Refrence number: A85480; MUID:21074935; PMID:11206551 A;Accession: H65719 A;Status: preliminary
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C;Superfamily: conserved hypothetical protein YEL070w
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0; Mismatches
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Pred. No.
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Matches 9; Conserv
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A; Residues: 1-488 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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                                                                                                                                                                                     Adatobable fructuronate reductase (EC 1.1.1.57) ydfI - Escherichia coli (strain K-12)
N.Alternate names: D-mannonate oxidoreductase
C.Species: Escherinia coli
C.Species: Escherinia coli
C.Bate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C.Accession: A64909
R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.; Tete: The complete genome sequence of Escherichia coli K-12.
A.; Reseince 177, 1453-1462, 1997
A.; Tete: The complete genome sequence of Escherichia coli K-12.
A.; Accession: A64909
A.; Status: nucleic acid sequence not shown; translation not shown
A.; Residues: 1-486 < BLAT>
A.; Residues: 1-486 < BLAT>
A.; Residues: 1-486 < BLAT>
A.; Residues: UNA
A.; Residues: U
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190897

probable oxidoreductase EC92151 [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli
C; Species: N: Yasungag, T:; Kuhara, S:; Shiba, T:; Hattori, M.; Yokoyama, K.; Han, C.G.
G; Stella: Camplete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Residues: 1-486 cHayy
A; Molecule type: DNA
A; Residues: 1-486 cHayy
A; Molecule type: Coli C Sibanon Coli O157:H7, Substrain RIMD 0509952
C; Genetics:
A; Gene: EC82151
C; Superfamily: conserved hypothetical protein YEL070w
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100.0%; Pred. No. 1.2;
iive 0; Mismatches
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100.0%; Pred. No. 1.2;
iive 0; Mismatches
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Matches 9; Conservative
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Matches 9; Conservative
183 AFTVMSCDNL 192
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Tyoung hydroxymethyltransferase (EC 2.1.2.1) - Corynebacterium sp. (fragment)
N.Alternate names: serine aldolase; serine hydroxymethylase; threonine aldolase
C;Species: Corynebacterium sp.
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 22-Jun-1999
C;Accession: I40886
R;Chlumsky, L.J.; Zhang, L.; Jorns, M.S.
J. Blol. Chem. 270, 18252-18259, 1995
A;Title: Sequence analysis of sarcosine oxidase and nearby genes reveals homologies w
A;Reference number: A57385; MUID:95355441; PMID:7543100
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C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 19-May-2000
C;Accession: S73429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RiHimmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon A;Reference number: S73327; MUID:97105885; PMID:8948633
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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A;Cross-references: EMBL:U23955; NID:g927587; PIDN:AAC43458.1; PID:g927588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: glyA
C;Superfamily: glycine hydroxymethyltransferase
C;Keywords: phosphoprotein; pyridoxal phosphate; transferase
F;60/Binding site: pyridoxal phosphate (Lys) (covalent) #status
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A;Genetic code: SGC3
C;Superfamily: Escherichia coli hypothetical protein ygaF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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           Pred. No. 7.1;
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                                         Mismatches
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           100.0%;
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A; Residues: 1-384 <HIM>
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Job time : 34 secs
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219 LAKADDFE 226
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Syford hypothetical protein - Synechocystis sp. (strain PCC 6803)
C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C; Accession: Syford
C; Yadan, A; Yamada, A; Yasuda
A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Reference number: Sford
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-253 < KANN
A; Residues: 1-253 < KANN
A; Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA18673.1; PID:g165376
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pypothetical protein Atu2229 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) (Species: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 (Speciession: Ab2850 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 #text_change 11-Jan-2002 #text_change, C.; Wood, G.E.; Chen, Y.; Woo, I.; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 #text_change, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Alauthers: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; PMID:11743193
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                                                                                   A;Cross-references: GB:AE007869; PIDN:AAK87971.1; PID:g15157379; GSPDB:GN00169
C;Genetics:
A;Gene: ARX_C_4053
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-244 <KUR>
A;Cross-references: GB:AEO08688; PIDN:AAL43218.1; PID:g17740700; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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tive 0; Mismatches
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0; Mismatches
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Best Local Similarity
Matches 8; Conserv
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-244 <KUR>
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"Cloning, nucleotide sequence and characterization of the mannitol dehydrogenase gene from Rhodobacter sphaeroides."; J. Gen. Microbiol. 139:2475-2484(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                112892 seqs, 41476328 residues
GenCore version
Copyright (c) 1993 - 2003
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WILK, RHOSH
WXUB_ECOLI
YDFI_ECOLI
YOFI_ECOLI
YORA_CORSI
YORA_CORSI
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Gapop 60.0 , Gapext 60.0
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Match Length DB
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Escherichia.
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                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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1-FEB-1995 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
D-mannonate oxidoreductase (EC 1.1.1.57) (Fructuronate reductase)
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                                         Schneider K.-H., Giffhorn F.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                 -!- SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY.
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100.0%; Pred. No. 0.0064;
ive 0; Mismatches 0; Indels
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Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mizobuchi K.;
Submitted (SEP-1992) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-mannonate + NAD(+) = D-fructur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 29 NAD (BY SIMILARITY).
476 AA; 51406 MW; A58247D6C7CCAF29 CRC64;
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InterPro; IPR000669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
PRIWTS; PR00084; WTLDHDRGNASE.
PROSITE; PS00974; MANNITOL_DHGENASE; 1.
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Matches 11; Conservative
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211 FPNGMVDRITP 221
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STRAIN-K12 / W3110;
SEQUENCE FROM N.A.
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STAIN-MILZ / MG1655,
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97251357; PubMed=9097039;
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Alba H., Rasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Moromura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
A 570-kb DNA sequence of the Escherichia coli K-12 genome Corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                                                                                                                                                              Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                NAD (BY SIMILARITY).
7835638682AF7B87 CRC64;
                                                                                                                                                                                                                                                                                                                                       DB 1; Ler
0.067;
thes 0;
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01-NoV-1997 (Rel. 35, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase ydfI (EC 1.-.-.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486 AA
                                                                                                                                                                                                                                                                                                                                                           100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                              Score 10;
Pred. No.
                                                                                                                                                                                PROSITE; PSO0974; MANNITOL DHGENASE; 1.
Oxidoreductase; NAD; Complete proteome.
NP_BIND 25 36 NAD (BY SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EcoGene, EG13821; ydfI.
InterPro, IPR000669; Mannitol_dh.
EMBL; AE000503; AAC77279.1; -.
BMBL; D1329; BAA02591.1; -.
ECOGENE; EG2248; uxuB.
InterPro; IPR000669; Mannitol_dh.
                                                                                                                                                                                                                                                                             486 AA; 53580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000251; AAC74615.1; -.
                                                                                                                                                       PRINTS; PRO0084; MTLDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                              2.18;
                                                                                                                          Pfam; PF01232; Mannitol_dh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D90797; BAA15243.1;
EMBL; D90798; BAA15247.1;
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3:363-377(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 KAFTVMSCDN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 KAFTVMSCDN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDFI OR B1542.
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DALD_YERPE
                                                                                                                                                                                            Y039_MYCPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95355441; PubMed=7543100;
Chlumsky L.J., Zhang L., Jorns M.S.;
Sequence analysis of sarcosine oxidase and nearby genes reveals homoLogies with key enzymes of folate one-carbon metabolism.";
J. Biol. Chem. 270:18252-18259(1995).
-!- FUNCTION: INTERCONVERSION OF SERINE AND GLYCINE.
-!- CATALYTIC ACTIVITY: 5. 10 -methylenetetrahydrofolate + glycine
H(2)O = tetrahydrofolate + L-serine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
27578 MW; AD16613C7DAE467B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34) Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: PYRIDONAL PHOSPHATE (BY SIMILARITY).
-!- PATHWAY: KEY ENZYME IN THE BIOSYNTHESIS OF PURINES, LIPIDS, HORMONES AND OTHER COMPONENTS.
                                                                                                                                                                                                                                                                                                                                                                                                            ó
Pfam; PF01232; Mannitol_dh; 1.
PRINTS; PR00084; MTLDHDRGNASE.
PROSTTE; PS00974; MANNITOL_DHGENASE; 1.
Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
Trunh 24 NAD (BY SIMILARITY).
C*685 NW; 96F3BF07AE114B70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 260;
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PROSITE; PS00096; SHMT; 1.
Transferase; Pyridoxal phosphate; One-carbon metabolism.
                                                                                                                                                                                                                                                                                                                                 Score 9; DB 1;
Pred. No. 0.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 AA
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100.0%; Pred. No. 4;
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-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE SHWT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001085; Gly_HyMetransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium sp. (strain P-1).
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U23955; AAC43458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 AFTVMSCDN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 AFTVMSCDN 184
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P50434;
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BINDING
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DD4CD
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MEDLINE-21470413; PubMed=11586360;
MEDLINE-21470413; PubMed=11586360;
MEDLINE-21470413; PubMed=11586360;
Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Fyersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                          "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
                                                                                                                                                           Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                            Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               il protein; Complete proteome.
384 AA; 42724 MW; DA3E128719EE1BCD CRC64;
                                                                                          (Rel. 40, Last annotation update) protein MG039 homolog (D09_orf384).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
D-arabinitol 4-dehydrogenase (EC 1.1.1.11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 8; DB 1;
Pred. No. 5.6;
384 AA
                                         (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000012; AAB95751.1; -.
InterPro; IPR000927; D_aa_oxidase.
Pfam; PF01266; DAO; 1.
Hypothetical protein; Complete prot
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE-97105885; Pubmed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5-JUN-2002 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
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STANDARD;
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                                                                                     (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11||||||
219 LAKADDFE 226
                                                                                                                                                                                                       NCBI_TaxID=2104;
                                                                                                                                        MPN051 OR MP103
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                                                                                                                  Hypothetical
                                           01-NOV-1997
01-NOV-1997
                                                                                            16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DALD_YERPE
P58709:
Y039_MYCPN
P75063;
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Gaps

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Indels

8; Conservative

Matches

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HSSP; P24666;
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052787;
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MUTAGEN
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              Query Match
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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ferrochelatase (EC 4.99.1.1) (Protoheme ferro-lyase) (Heme synthetase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions on
ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 175:1412-1422(1993).
-!- FUNCTION: CATALYZES THE FERROUS INSERTION INTO PROTOPORPHYRIN IX.
-!- CATALYICA ACTIVITY: Protoporphyrin + Fe(2+) = protoheme + 2 H(+).
-!- PATHWAY: Protoheme biosynthesis; last step.
-!- PATHWAY: Protoheme Subsynthesis; last step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE FERROCHELATASE FAMILY.
                                                                                                                                                                                                                                                                                                   Gaps
CATALYTIC ACTIVITY: D-arabinitol + NAD(+) - D-xylulose + NADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yersinia pseudotuberculosis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                   ó
              -!- PATHWAY: D-arabinitol catabolism; first step. -!- SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kessler A.C., Haase A., Reeves P.R.; "Molecular analysis of the 3,6-dideoxyhexose pathway genes of
                                                                                                                                                                                                                                                                     Length 463;
                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfan, PF00762; Ferrochelatase, 1.
ProDom; PD002792; Ferrochelatase; 1.
PROSITE; PS00534; FERROCHELATASE; PARTIAL.
Porphyrin biosynthesis; Heme biosynthesis; Lyase; Iron.
                                                                                                                                                                                                                                         D82E8988685B5EDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRON (BY SIMILARITY).
5E3D1BA7AFACDE5E CRC64;
                                                                                                                                                                                InterPro; IPR000669, Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
PROSITE; PS00974; MANNITOL_DHGENASE; FALSE_NEG.
                                                                                                                                                                                                                                                                    1.6%; Score 8; DB 1;
100.0%; Pred. No. 6.6;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yersinia pseudotuberculosis serogroup IIA.";
                                                                                                                                                                                                                                                                                                                                                                                                                             77 AA.
                                                                                                                                                                                                                            Oxidoreductase; NAD; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001015; Ferrochelatase.
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                                                                                                                                                                                                                                         51984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 AA; 8766 MW;
                                                                                                                                                                      EMBL; AJ414152; CAC91130.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L01777; AAB49397.1; -
                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                           463 AA;
                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             168 CDNLRHNG 175
                                                                                                                                                                                                                                                                                                                            188 CDNLRHNG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=633;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Fragment).
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Q05338;
                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yersinia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphotyrosine-protein phosphatase of Adinetobacter johnsonii.";
J. Mol. Biol. 278:339-347(1998).
-:-FONCTION: Dephosphorylates ptk. May be involved in the production and the transport of exopolysaccharides.
-:-CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
-:-ENZYME REGULATION: Inhibited by ammonium molybdate, sodium orthovanadate, N-ethylmaleimide and iodoacetic acid.
-:-PATHWAY: Exopolysaccharide biosynthesis.
-:-SIMILARITY: BELONGS TO THE LOW MOLECULAR WEIGHT PHOSPHOTYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duclos B., Cozzone A.J.;
"Characterization of a bacterial gene encoding an autophosphorylating
protein tyrosine kinase.";
Gene 204:259-265(1997).
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Low molecular weight protein-tyrosine-phosphatase ptp (EC 3.1.3.48).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grangeasse C., Doublet P., Vaganay E., Vincent C., Deleage G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTON DONOR (BY SIMILARITY).
C->S: LOSS OF ACTIVITY.
R->K: LOSS OF ACTIVITY.
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ACT_SITE 10 10 NUCLEOPHILE (BY SIMILARITY).

ACT_SITE 15 15 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 142;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION, AND MUTAGENESIS OF CYS-10 AND ARG-16.
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1.4%; Score 7; DB 1;
100.0%; Pred. No. 14;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                 142 AA
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100.0%; Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98239739; Pubmed~9571056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98094281; PubMed=9434192;
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                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
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16215 MW;
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                                                             Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acinetobacter johnsonii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01451; LMWPC; 1
SMART; SM00226; LMWPC;
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                           Best Local Similarity
Matches 7; Conserv
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                                                                                                                     5 ETLKSLP 11
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ETLKSLP 12
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YPIB_BACSU
P54390;
                                                                                                                                                                                                                                                                                                                                                                                    Serror P.;
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                                                                                                                                            Query Match
                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the SAISS Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                              "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MG428 homolog (Cl2_orf172).
MPN626 OR MP216.
Mycoplasma pneumoniae.
Bacteria, Firmicutes; Mollicutes; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                            Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 171; . 28;
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000792; HTH_LuxR.
Hypothetical protein; Complete proteome.
SEQUENCE 171 AA; 20259 MW; 87FB346C334E5E72 CRC64;
                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                     171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Score 7; 1
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                    PRT;
                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed=756993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                             1.4%;
                                                                                                                                                                                                                                                                                                                                                       EMBL; U39725; AAC72449.1; -
                                                                                                               Hypothetical protein MG428
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.4
Best Local Similarity 100.
Matches 7; Conservative
                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                   Mycoplasma genitalium.
      239 IAKKLNA 245
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|139 EIAKKLN 145
                                                                                                                                                    NCBI_TaxID=2097;
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                TIGR; MG428;
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ID Y428_MYCPN
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A Zevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Borriss R., Boursier L., Brans A., Brans A., Brans A., Brons. Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.E., Cummings N.J., Daniel R.A.,
A benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
A Parro V., Pohl T.M., Porterelle D., Porwollik S., Parksort A.M.,
Parro V., Pohl T.M., Porterelle D., Porwollik S., Parksort A.M.
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Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roshe B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=168 / Marburg;
MEDLINE=96349105; PubMed=8760912;
Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 172;
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NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000021; AAB95864.1; -.
InterPro: IPR000792; HTH_LuxR.
Hypothetical protein; Complete proteome.
SEQUENCE 172 AA: 20473 MW; 93F6430F3BF8C4AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
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100.0%; Pred. No. 28;
ative 0; Mismatches
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pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sest Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
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01-OCT-1996 (
15-JUN-2002 (
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RESULT 14
DGC6_CHICK
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Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yashida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus subtills",
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stevenson G., Andrianopoulos K., Hobbs M., Reeves P.R.; "Organization of the Escherichia coli'K-12 gene cluster responsible for production of the extracellular polysaccharide colanic acid."; J. Bacteriol. 178:4885-4893(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-M12 / MG1655.
STRAIN-M27426617. PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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P17240; P76383;
P1-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative colanic acid biosynthesis acetyltransferase wcaF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                     Length 179;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                         EMBL; 299115; CAB14174.1; -.
Subtilist, BG11497; ypiB.
Hypothetical protein; Complete proteome.
SEQUENCE 179 AA: 21364 MW; 46366E994DB709D9 CRC64;
                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                    Score 7; DB 1
Pred. No. 29;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96326333; PubMed-8759852;
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MEDLINE=97251358; PubMed=9097040;
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100.0%; Pir
0;
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                                                                                          Nature 390:249-256(1997)
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                                                                                                                                          137 EQILEHA 143
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                                                                                                                                                                                                                                                                                                                                   EQILEHA 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-K12;
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Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; Repeat;
                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF THE SLIME POLYSACCHARIDE
                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makin T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasuudaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T., "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DGCR6 protein (DiGeorge syndrome critical region 6 homolog).
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SERANI=Broiler; TISSUB=Heart;
Hierck B.P., Poelmann R.E., Gittenberger-De Groot A.C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO THE GONADAL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F -> L (IN REF. 2).
; 8AA5E672CA802442 CRC64;
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Mismatches
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19962 MW;
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EMBL, D90843, BAA15910.1, -.
EcoGene, EG13574, wcaF.
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Best Local Similarity
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                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
GSTD1 OR GST.
Drosophila erecta (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecti; Pterrygota; Neoptera; Endopterrygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hargis M.T., Cochrane B.J.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
-!- CATALTIC ACTIVITY: RX + glutathione = HX.+ R-S-glutathione.
-!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. THETA FAMILY.
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01-APR-1993 (Rel. 25, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
Glutathione S-transferase 1-1 (EC 2.5.1.18) (GST class-theta)
                                                                                         Length 200;
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COILED COIL (POTENTIAL).
7037BBF6F660E469 CRC64;
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5. 32;
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Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches
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                                                                                         Ouery Match 1.4%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches
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InterPro; IPR004046; GST_Cterm.
Coiled coil.

DOMAIN 116 146 CC

DOMAIN 176 198 CC

SEQUENCE 200 AA; 23242 MW;
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Pfam; PF02798; GST_N; 1.
                                                                                                                                                            462 ELDQKVI 468
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Search completed: May 8, 2003, 16:42:56 Job time: 17 secs

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Q9kwr5 gluconobact
Q8vuu5 gluconobact
Q8Nu13 gaycobacteri
Q8N13 gaycobacteri
Q8000 rhizobium 1
Q92n07 rhizobium 1
Q92n07 rhizobium 1
Q9x16 escherichia
Q9x16 escherichia
Q8x50 escherichia
Q8x50 salmonalla
Q8x50 salmonalla
Q8x60 synechocyst
Q9x439 drosophila
Q8v439 drosophila
Q8v4392 borrelia ga
Q8vup2 ralstonia s
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1122.841 Million cell updates/sec
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                 671580 seqs, 206047115 residues
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                                             OM protein - protein search, using sw model
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Q8U7J8
Q8U7J8
Q9ZN07
Q8X516
Q911D6
Q8X506
Q8XF06
Q8XP18
Q8XP18
Q9W439
Q24792
Q8XUP2
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Gapop 60.0 , Gapext 60.0
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sp_rodent:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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sp_mhc:*
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ALIGNMENTS

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OR ATU4451 OR AGR_L_830
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"NADPH-Dependent L-Sorbose Reductase Is Responsible for L-Sorbose Sasimiation in Glucomobacter suboxydans IFO 3291.";
J. Bacteriol. 184:861-863(2002)
EMBL, AB063188; BAB83933.1;
InterPro; IPR000669; Mannitol_dh.
PRINTS; PR00084; MAIDHDGANASE
SEQUENCE 485 AA; 53541 MW; 883EC4956B3C6CFO CRC64;
 PAIRIVSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGG
                    GHVMLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISR
                                                                                                                                                                                                                                          FSNKAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKG
                                                                       KAFTVMSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIA
                                                                                                                                               KKLNAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNA
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Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
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MEDLINE=21650687; PubMed=11790761;
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01-MAR-2002 (TrEMBLrel.
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Best Local Similarity
Matches 52; Conserv
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NCBI_TaxID=442;
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Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamotó S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21008551; PubMed-11743194; Goodner B., Hikle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmtel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
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                                                                                                                             BEQUENCE FROM N.A.

MEDLINE=2160856): PubMed=11743193;

Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Mood D.W., Setubal J.C., Kaul R., Mood G.E., Almeida M.F. Jr., Moo L.,

Choura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Lewy R., Li M.-J., McClelland E., Palmieri A. G.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon L.

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Condon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Mester E.W.;
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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Last annotation update)
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Pred. No. 0.00027;
0; Mismatches 0;
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EMBL; AE008240; AAK88989.1; -
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100.0%; Pre-
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DNA Res. 7:31-338(2000).
EMBL; AP003005; BAB51465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens C5
Science 294:2323-2328(2001).
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                                                                   Rhizobium.
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MEDLINE=21074935; PubMed=11206551;
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MEDLINE=21396507; PubMed=11481430;
MEDLINE=21396507; PubMed=11481430;
MEDLINE=21396507; PubMed=11481430;
MEDLINE=21396507; PubMed=11481430;
Boistard P., Backer A., Goutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Godrie T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
EMBL: AL591790; CAC47019.1; -
InterPro. IPR000669; Mannitol_dh.
                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TIEMBLE1. 19, Created)
01-MAR-2002 (TIEMBLE1. 19, Last sequence update)
01-MAR-2002 (TIEMBLE1. 20, Last annotation update)
Probable mannitol 2-dehydrogenase protein (EC 1.1.1.67).
RHIK OR RO2440 OR SMC01501.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Mannonate oxidoreductase (D-mannonate oxidoreductase)
UXUB OR 25921 OR EC55282.
Escherichia coli 0157:H7.
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                                                                                                                                      2.3%; Score 11; DB 16;
100.0%; Pred. No. 0.03;
iive 0; Mismatches 0;
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PROSITE; PS00974; MANNITOL_DHGENASE; UNKNOWN_1.
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Pred. No. 0.03;
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                                                         PROSITE; PS00974; MANNITOL_DHGENASE; 1.
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InterPro; IPR000669; Mannitol_dh.
                                        PRINTS; PR00084; MTLDHDRGNASE
                                                                                                                                                                                     Conservative
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                                                                                                                                                           Best Local Similarity
Matches 11; Conserv
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MEDLINE=21156231; PubMed=11258706;
Haydshi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Haydshi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe T., C., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Sasunaga T., "Complete genome sequence of enterchemorrhagic Escherichia coli O15:H7 and genomic comparison with a laboratory strain K-12.";
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MEDLINE=2043733; PubMed=10984043;
Stover C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Bosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of entrohagic Escherichia coli ol57:H7."; Nature 409:529-533(2001).
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Pseudomonas.
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Pred. No. 0.32;
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Last annotation update)
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InterPro; IPR000669; Mannitol_dh.
Prim; PF01322; Mannitol_dh; 1.
PRINTS; PR00084; MTLDHDRGNASE.
PROSITE; PS00974; MANNITOL_DHGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan; PF01232; Mannitol dh; 1.
PRINTS; PR00084; MTLDHDRGNASE.
PROSITE; PS00974; MANNITOL_DHGENASE; 1.
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                                                                                                                                                                                                                                                                                                                         STRAIN=0157:H7 / RIMD 0509952;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 KAFTVMSCDN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 10; Conserv
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 206:117-126(1998).

-!- FUNCTION: A MANNITOL DEHYDROGENASE WITH A BROAD SUBSTRATE SPECIFICITY. SUBSTRATES INCLUDE MANNITOL, ARABITOL AND SORBITOL, THESE ARE OXIDIZED TO GIVE THE CORRESPONDING KETO SIGARS. THIS ENZYME WILL ALSO CATALYZE THE REDUCTION OF FRUCTOSE AND XYLULOSE.
-!- CATALYTIC ACTIVITY: D-MANNITOL + NAD(+) = D-FRUCTOSE + NADH.
             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Bruenker P., Altenbuchner J., Mattes R.; "Structure and function of the genes involved in mannitol, arabitol and glucitol utilization from Pseudomonas fluorescens DSMS0106.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBUNIT: MONOMER.
-i- INDUCTION: BY MANNITOL, ARABITOL AND SORBITOL. NOT INDUCED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: THE WILD PROTEIN IS ENCODED BY THE MIL EFGKDYZ OPERON. THIS OPERON ENCODES PROTEINS FOR THE UPTAKE AND UTLIZATION OF MANNITOL, ARBHITOL AND SORBITOL.
-!- SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY.
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                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                     Bruenker P., Altenbuchner J., Kulbe K.D., Mattes R.; "Cloning, nuclectide sequence and expression of a mannitol dehydrogenase gene from Pseudomonas fluorescens DSM 50106 in Escherichia coli.";
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., CHARACTERIZATION, AND SEQUENCE OF 1-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 10; DB 2; Length 493; 100.0%; Pred. No. 0.32;
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             Indels
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7C12DFA443CEA443 CRC64;
                                                                                                                                                 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Mannitol 2-dehydrogenase (EC 1.1.1.67) (MDH).
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  Pred. No. 0.32;
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                                                                                                                 493 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
              Mismatches
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PROSITE; PS00974; MANNITOL_DHGENASE; 1.
Oxidoreductase; NAD.
19 40 NAD (BY SI)
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                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98121321; PubMed=9461423;
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MEDLINE-97236441; PubMed-9116029;
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100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
             10; Conservative
                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                Pseudomonas fluorescens
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                                                182 AFTVMSCDNL 191
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                                  182 AFTVMSCDNL 191
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  NCBI_TaxID=294;
                                                                                                                                        01-JUL-1997
01-JUL-1997
                                                                                                                                                                                                                        Pseudomonas
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Q8X506;
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008355
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Q8X506
ID Q8X50
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli
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                                                                                                                                                                                                                                                          STRAIN-0157:H7 EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
MEDLINE-21074935; PubMed-11206551;
MEDRINE-21074935; PubMed-11206551;
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim, A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0157:H7 and genomic comparison with a laboratory strain K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486 AA; 53581 MW; 1AFD234D83108D9E CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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; Mismatches
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PROSITE; PS00974; MANNITOL_DHGENASE; 1.
COMPlete protecome.
SEQUENCE 486 AA; 53581 MW; 1AFD234DE
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MEDLINE=21534948; PubMed=11677609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 8:11-22(2001).

EMBL; AE005350; AAG56220.1; -

EMBL; AP002557; BAB35574.1; -

InterPro; IPR000669; Mannitol_dh.

Pfam; PF01232; Mannitol_dh; 1.
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                               YDFI OR 22155 OR ECS2151
Escherichia coli 0157:H7
Putative oxidoreductasė.
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                                                                                                                                                                   NCBI_TaxID=83334;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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P74566;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Daviss R.M., Dowd L., White N., Farrar J., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parrar J., Whitehead S., Barrell B.G., Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G., Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G., Multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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0
                                                                                                      1.9%; Score 9; DB 16; Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.9%; Score 9; DB 16; Length 488; 00.0%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primi: PRODOG4: WTLD-DRGNASE.
PROSITE: PS00974; MANNITOL_DHGBNASE; 1.
Oxidoreductase; Hypothetical protein; Complete proteome.
SEQUENCE 488 AA; 53922 WW; 18F64DEZACCA7781 CRC64;
                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                             PRINTS; PRO0084; WTLDHDRCNASE.
PROSTIE; PS00974; MANUTOL_DHGENASE; 1.
HYPOTHELICAL PROTEIN; COMPLETE PROTECOME
SEQUENCE 488 AA; 53896 MW; 704BPBC27F4407A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
AEC transporter, substrate binding protein.
ATU2229 OR AGR_C_4053.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
U-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative D-mannonate oxidoreductase (EC 1.1.1.57).
                                                                                                                   Pred. No. 3.4;
                                                                                                                                                                                                                                 488 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 AA.
                                                                                                            100.0%; Pred. ....
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                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21534947; PubMed=11677608;
Nature 413:852-856(2001).

EMBL; AE008765; AAL20427.1; -.

InterPro; IPR000669; Mannitol_dh.

Pfam; PF01222; Mannitol_dh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AL627270, CA001805.1; -.
InterPro: IPR000669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                  182 AFTVMSCDN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 AFTVMSCDN 190
                                                                                                                                                                         176 AFTVMSCDN 184
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                       Salmonella.
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08UD98
1D 08UD9
DT 01-JU
DT 01-JU
DT 01-JU
DE ABC t
GN ATU22
OS AGTOD
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Q82626
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"The genome of the natural genetic engineer Agrobacterium tumefaciens
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                                                                                                                                 MEDLINE=2160856; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Millol P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 8; DB 16; Length 244;
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Hypothetical protein; Complete proteome.
SEQUENCE 253 AA; 28428 MW; F836F5042295F03B CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein slr0654.
SLR0654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No. 19; ive 0; Mismatches
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MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 294:2323-2328(2001).
EMBL; AE009172; AAL43218.1; -.
EMBL; AE008138; AAK87971.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294:2317-2323(2001).
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Rhizobium
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SEQUENCE FROM N.A.
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SEQUENCE 244 AA;
                          NCBI_TaxID=176299;
                                                                                                          SEQUENCE FROM N.A.
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RECEIVED-20196006; Pubmed=10731132;
RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
ROOTER R.A., Lewis S.E., Richards S., Rabburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Adril J.F., Agabayani A.A. An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Adril J.F., Agabayani A.A. An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Benasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Borchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Bulke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.F., Houston B.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.F., Houston J.A.,
RA Harris N.L., Harvey D., Radi G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Harris N.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Harkon O., Kradt C., Kravitz S., Kulp D., Lai Z.,
RA Harkon O., Rillshina N.Y., Modarit Z., Nortis J., Moshrefi A.,
RA Harkon O., Rolson K.A., Li Y., Muzny D.N., Nelson D.L.,
RA Harkon O., Pittman G.S., Pollard J., Muzny D.N., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pollard J., Muzny D.N., Nelson D.L.,
RA Reinert K., Remington K., Saupeson M., Stupski M.P., Sanith T.,
RA Shier E., Spradling A.C., Stapletton M., Strong R., Sanith T.,
RA Merkulov S., Miller R., Weinstor R., Weinsen D.R., Wallishne R., Weinsen P., Wein R., R., Williams S., Walliams R., Walliams R., Walliams R., W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
   DB 16; Length 253; . 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.6%; Score 8; DB 5; Length 261; 100.0%; Pred. No. 21;
                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   261 AA
1.6%; Score 8; DB 1
100.0%; Pred. No. 20;
ive 0; Mismatches
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InterPro; IPR000365; 4HBcoA_thiostrse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                  Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
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                                                                                                                                              338 VIPTLKAP 345
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                                                                                                                                                                                            2 VIPTLKAP 9
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SEQUENCE 26
   Query Match
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Q9W439
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                                                                                                                                                                                                                                                                                                                                    Fukunaga M., Yabuki M., Nakao M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO07099; BaAA22341.1; -
HSSP: P14013; 10SP.
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28671 MW; 7405E3CEB928EF08 CRC64;
                                                                                                                                                                  05, Created)
05, Last sequence update)
17, Last annotation update)
                                                                                                                                                                                                                                                      Bacteria: Spirochaetales; Spirochaetaceae; Borrelia
NCBL_TaxID=29519;
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red. No. 21;
Mismatches
                                                                                                                                         264 AA
   Mismatches
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Pred. No.
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                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO01809; Outrsurface.
Pfam; PF00820; Lipoprotein_1; 1.
PRINTS; PR00968; OUTRSURFACE.
Probom; PD001127; Outrsurface; 1.
NON_TER 264 264
SEQUENCE 264 AA; 28671 MW; 740
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   0;
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Matches. 8; Conservative
   Conservative
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                    01-JAN-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Scoring table:

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Novel human diagno Human novel polype Streptococcus poly

Novel human diagno Putative P. abyssi Lactococcus lactis

Saito Y;

WPI; 2000-587530/55 N-PSDB; AAA97430

Enterococcus faeca E. coli cellular p Mannitol-1 dehydro

AAU34792 AAR28826

ABG13869 AAU35002

100.0 85.2 31.9 31.9 16.7 14.5 12.4 8.8

802 802 802 365.5 312.5 221.5 205 203

Score 2516 2143

Result ٠ 9 Yamashita M,

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D-sorbitol dehydrogenase; SLDH; L-sorbose production; NADP+ dependent; sorbitol; mannitol; arabitol; oxidation; 2-keto-L-gluconic acid; L-ascorbic acid biosynthesis; vitamin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gluconobacter oxydans D-sorbitol dehydrogenase (SLDH).
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99JP-0224679.
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, Takata Y;
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06-AUG-1999;
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1 MITRETLKSLPANVQAPPYD.......KVIVLRKIIREKGVKAAIPA 485
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Copyright (c) 1993 - 2003
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The invention relates to Gluconobacter oxydans D-sorbitol dehydrogenase (SLDH; AAB31372) and to the gene encoding it (AAA97430). SLDH has a molecular weight of about 54 kDa and catalyses the conversion of molecular weight of about 54 kDa and catalyses the conversion of D-sorbitol into L-sorbose using NADP+ as a co-enzyme. SLDH specifically catalyses the oxidation of sorbitol, mannitol and arabitol, but does not act on xylitol, ribitol, inositol and glycerol. The invention also compasses expression vectors and host cells comprising the Gluconobacter oxydans SLDH gene, and the recombinant production of SLDH. The invention further relates to a method for preparing L-sorbose by contacting the recombinant SLDH with D-sorbitol; a process for producing 2-keto-L-gluconic acid by contacting recombinantly produced sorbose dehydrogenase and/or sorbosone dehydrogenase with L-sorbose; and a process for preparing L-sorbose cataly for producing by conversion from 2-keto-L-gluconic acid. SLDH is useful for producing L-sorbose or 2-keto-L-gluconic acid as an intermediate in L-ascorbic
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                 culturing its gene-transformed host cells, useful for producing L-sorbose or 2-keto-L-gluconic acid as an intermediate in L-ascorbic
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derived D-sorbitol dehydrogenase obtainable by
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                                                                               Claim 5; Page 58-60; 72pp; Japanese
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 Gluconobacter oxydans
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Set of genetically modified mutants not containing L sorbose reductase
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                                                                                                                                                                                                                                                                                                                                                                                   biological activity for reducing L-sorbose is substantially nullified by gene recombination gene. The present sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                         Gluconobacter suboxydans L-sorbose reductase.
N.B. This patent is equivalent to the basic NO9901197 in week 199949.
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                                                          suboxydans; L-sorbose reductase; genetic engineering;
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                                                                                                                                                                                                                                                                                                                                                            microorganism derived from a microorganism belonging to the Gluconobacter or Acetobacter which is characterised in that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                 suboxydans L-sorbose reductase protein
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Pred. No. 5e-187;
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                                                                                                                                                                                                                                         Kon
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                                                                                                                                                                                                                                         Shinjoh M,
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84.5%;
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           (first entry)
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Matches 410; Conserv
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                                  Gluconobacter
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         27-JAN-2000
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AAY49913;

AAG89872;

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Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; proteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                  67. IGMGVMPSDVRMRDA--LASQDHLYTLTTKAPDGTLDQKIIGSIIDYVFAPEDPARAVAT 124
                                                        PTVS---AEIAKKLNAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTD
                                                                                                                                                                                                       290 WEYVKIRMLNAGHVMLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMT
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| 421 ARYAEGTDEQG 431
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14-JUL-1999;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. The are useful for identifying the mutation point of a gene derived from a
421 GTYEPFEPTFGDNHKTLAKADDFESALKLPAFDAWRDLETSGLNNKVVELRKIIREKGVK 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotides derived from Coryneform bacteria, for identif mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yokoi
                                                                                                                                                                                                                                                                                                         Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                                                                                       glutamicum protein fragment SEQ ID NO: 3626.
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2000JP-0159162.
2000JP-0280988.
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03-AUG-2000;
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Nakagawa Tateishi

Sequence

Query Match Best Loca Matches

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AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar metabolism and oxidative phosphorylation (SMP) proteins given in AAB79433 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors cenergy production of fine chemicals, such as, an organic acid, a proteinogenic cor nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty cor nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corraining them are used for as subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to interest, or evolutionary studies, in determining SMP protein regions required for for function, in modulating SMP protein activity, in modulating the mace metabolism of sugars, and in modulating high-energy molecule production con a cell (i.e. ATP, NADPH).
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                                                                                                                                                                                                                                                                                                            New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAQDSIRIVSLTVTEGGYNIDPATEDFDHTNPRIVADREALQAGDTSTLQTFFGLITAAL
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39.0%; Pred. No. 2.3e-64;
ive 82; Mismatches 163;
                                                                                                                                                                                                                           Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 615-616; 1246pp; English.
                                                                                                                                                                                                                         Schroeder H,
              99US-0151572.
99DE-1042076.
99DE-1042079.
                                                              99DE-1042086.
99DE-1042087.
99DE-1042088.
99DE-1042095.
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99DE-1042125
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Matches 168; Conservative
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                31-AUG-1999;
03-SEP-1999;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by c. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lessions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contecting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the vipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzymelinked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                         for
LEGYRDSVISRFSNKAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes immunogenic protein #709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DH, Mitcham JL, Wang St
ang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID No 1008; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       AAU39813 standard; Protein; 534 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000, 2000US-199047P.
02-JUN-2000, 2000US-208841P.
07-JUL-2000, 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes.
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                                                                                                                                                                                                                    421 ARYAEGTDEQG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-616774/71.
N-PSDB; AAS59508.
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                                                                                                                                                410 LEMLRGRDEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU39813;
350
                                                                                                                                                                                                                                                                                                                                   RESULT 5
AAU39813
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534 AA;

Sequence

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16;

71;

Mon

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nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related sepecies. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                           LKHLV----DPAIRIVSMT1TEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVE 170
                                                                                                                                                                                                                                                                                                                                                                  ---ENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLVA------EDFHQW 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLEDQFADGRPPLEKAGVQMVG--DVTDWEYVKI-RMLNAGHVMLCFPGILVGYENVDDA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVIS-RFSNKAMSDQTLRIASDGCS 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVQVFWTETVRRAIEDKR----DLSRIAFGIASYLEMLRG-RDEKGGTYESSEPTYGDAE 434
                                                                                                                                                                                                                                                                                          WAIVGVGLTGSDRSKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADPEAV 114
                                                                                                                                                                                                                                                  1 MITRETLKSLPANVQAPPYDIDGI-----KPGIVHFGVGNFFRAHEAFYVEQILEHAPD 54
                                                                                                                                                                                                                                                                                                                                                                                                                            171 ALRRRWDAGGKAFTVMSCDNLRHNGNVARKAFLGYAKARDPELAKWIE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIPVRYGVTIGHYIANPRFSVKELEFIPLVIAAWCRYLIGINDELESFSPSPDPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                          Length 544;
                                                                                                                                                                                                       Indels
                                                                                                                                                                         Score 365.5; DB 23;
Pred. No. 2.1e-24;
I; Mismatches 213; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #13860.
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                                                                                                                                                                                                     84;
                                                                                                                                                                         14.5%;
26.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                        Best Local Similarity
Matches 132; Conserv
                                                                                                                                               544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200175067-A2
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                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                  115
                                                                                                                                                                                                                                                                                                                                                                                                                                    182
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                                            14;
                                                                                                                                               GKAFTVMSCDNLRHNGNVARKAFLGYAK-----ARDPELAKWIEENATFPNGMVDRITP 233
                                                                                                                                                                                                                                                               TVSAEIAKKLNAAS----GLDDDLPLV----AEDFHQWVLEDQFADGRPPLEKAGVQMVG 285
                                                                                                                                                                                                                                                                                                                                                            DVTDWEYVKIRM---LNAGHVMLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                     SDRSKKKAEEFKAQDCLYSLTETA-PSGKSTVRVMGALRDYLLAPADPE--AVLKHLVDP 121
                                                                                                                                                                                      AIRIVSMTITEGGYNINETTGAFDLENAAVKADLKNPE--KPSTVFGYVVEALRRRWDAG 179
                                                                                                                                                                                                                                                                                                                                255 APSOKVAEQLAAMGLEDMGIDPDVEVAGFVNTEPAEYLVIEDRFPNGRPELEKAGVYFTD 314
                                                                                                                                                                                                                                                                                                                                                                                      315 RDTCYRFERMKVTTCLNPLHTALAITGVLLRKPTIDEAMKDPGLAGLVHCLGWQEGLPVV 374
                                            Gaps
                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide
                                                                    12 ANVQAPPYDIDGI-----KPGIVHFGVGNFFRAHEAFYVEQILEH-APDWAIVGVGLTG
                                                                                                                                                                                                                                                                                                                                                                                                                   KAPSGM-TLEGYRDSVISRFSNKAMSDQTLRIASDGCSKVQVFWTETVRRAIEDK----R
                                                                                               AGLALPLFDVGEMRSQAHDRPRWMHIGPGNLFRVHIARLAQDIMNSGAEQCGIAAI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention is related to a Lactococcus lactis nucleotion sequence (ABB490521) and related proteins (ABB53300-ABB55621). The
                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                534;
              Length
                                            Indels
                DB 22;
                                         199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlich SD;
             Score 419.5; DB 2
Pred. No. 2.4e-29;
); Mismatches 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLRAIPFVFAAWCRYLMGIADDGEPVELSSDPLLGQLE 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398 DLSRIAFGIASYLEMLRGRDEKGGTYE-SSEPTYGDAE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; SEQ ID No 1680; 2504pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB54978 standard; Protein; 544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis protein uxuB.
                                         90;
             16.7%;
27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2000; 2000FR-0004630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lactis and related species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                            cal Similarity 27.9
128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorokine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-043418/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2001
                Query Match
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                             Local
                                        Matches
                                                                                                                            65
                                                                                                                                                                                     122
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ABB54978
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Carr GJ;

Trawick JD,

Wall D,

Ohlsen KL, Zyskind JW, Xu HH;

2000US-242578P. 2000US-253625P. 2000US-257931P. 2001US-269308P.

2000US-206848P. 2000US-207727P.

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21-MAR-2001; 2001WO-US09180.
                                                                                                                                                                                                                 (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                       2001-611495/70.
                                                                                                                                                                                                                                                                                                    N-PSDB; AAS52861.
             WO200170955-A2
                                                                                                                                                                                                                                             Haselbeck R,
                                                                                                                                                                       22-DEC-2000;
16-FEB-2001;
                                                                                                                                           23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                              Yamamoto RT,
                                                                                                                               26-MAY-2000;
                                                                                                                 23-MAY-2000;
                                           27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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  δλ
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                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human man and amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 LVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGY 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 QHINDCMEDEHYRYAAYGLMLQEQAPTLKV-QGVDLQDYANRLIARYSNPALRHRTWQIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 ENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRFSNKAMSDQTLRIA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VACEPFRQWVIEDNFVAGRPEWERAGAELVSDVLPYEEMKLRMLNGSHSFLAYLGYLAGY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDGCSKVQVFWTETVR--RAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYESSEPTY 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis cellular proliferation protein #289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.4%; Score 312.5; DB 22;
llarity 37.6%; Pred. No. 2.6e-19;
Conservative 37; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                             Claim 20; SEQ ID No 44228; 103pp; English.
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                                                                                   Tang YT;
             31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                   Liu C,
                                                                                                                WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            788 AA;
                                                        (HYSE-) HYSEQ INC
                                                                                                                               N-PSDB; AAS78056
                                                                                                                                                                                                   biodiversity
                                                                                   Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes, their use in the discovery of novel antibiotics, the essential genes, their use in the discovery of novel antibiotics, the essential genes, themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureaus, Salmonella typhi, Klebsleila pneumoniae, Pseudomonas acruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets in antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Contact The sequence data for this patent did not form part contactive for the printed specification, but was obtained in electronic contactive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 AAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKA-----FTVMSCDNLRHNGNVARKAFL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENV 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 123; Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 VHFGVGNFFRAHEAFYVEQILEHAPDWAIVGVGLTGSDRSKKKAEEFKAQDCLYSLTETA 88
                                                                                                                                                                                                                      essential to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 384;
polynucleotides for the identification and development of biotics, comprise sequences of antisense nucleic acids -
                                                  antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                      invention relates to antisense inhibitors of genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VHFGAGNIGRG----FIGEIL-----AKNGFHITFVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 221.5; DB 2
Pred. No. 1.8e-11;
                                                                                                                               Example 3; Seq ID No 10595; 511pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expresse proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a widely acids and antibodies and the prosent sequence represents an acceptance and the prosents and the proper provides and the prosents and the p
    ---EGYRDSVISRFSNKAM 366
                          Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotides for the identification and development of
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Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiblotics, comprise sequences of antisense nucleic acids
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                                                                                                                                                                                                                                                                                                                                                        coli cellular proliferation protein #373.
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  DDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTL-
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Xu HH;
                                                                                                                                                                                                                                AAU34792 standard; Protein; 382 AA
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2000US-207727P.
2000US-242578P.
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2000US-257931P.
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                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                  SDQTLRIA 374
                                                                                                                        SDAITRVA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
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23-OCT-2000;
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22-DEC-2000;
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                                                                                                                                                                                                                                                                                                                 14-FEB-2002
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318
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AAU34792
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320
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                                 Gaps
                                                                                  29 VHFGVGNFFRAHEAFYVEQILEHAPDWAIVGVGLTGSDRSKKKAEEFKAQDC--LYSLTE 86
                                                                                                                                                                                                                                                                                                                       QWVLE-DQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDA
                                                                                                                                                                                                                                                                                                                                           54 TEQVDTVSGVNAVSSIGDDVVDLIAQVD-----LVTTAV-----G
                                                                                                                                                                                                                        89 PVVLERIA-----PAIAKGOV----KRKEQGNESPLNIIACENM-VRGTTQLK--
                                                                                                                                                                                                                                                         203 LGYAKARDPELAK-WIEENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLVAEDFH
                                                                                                                                                                                                                                                                                                                                                                                       321 IEDSELLGNLKNYLNKDVIPTLKAPSGMTL------EGYRDSVISRFSNKAMSDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 KNLIE-GIAAAMHFR------SEDDPQAQELAALIADKGPQAAL 358
                               71; Mismatches 161; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 YGDAEWKLAKADDFESSLKLPAFDGWRDLDTSELDQKVIVLRKIIREKGVKAAI 483
   Length 382;
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Score 205; DB 22;
Pred. No. 5.8e-10;
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myo-inositol O-methyl transferase.
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                               Conservative
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N-PSDB; AAQ31199.
               Similarity
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Query Match
Best Local Simi
Matches 104;
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Tang YT;

Liu C,

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WPI; 2001-639362/73
                                             N-PSDB; AAS92760
           Drmanac RT,
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                    Two separate genes are capable of inducing novel polyol biosynthesis in transgenic plants. One gene is bacterial in origin, e.g. E. coli derived mtlD encoding mannitol-1-P dehydrogenase (AAQ31199). The gene for this enzyme has been described by Lee and Saier, J. Bact., 153:2, 685-692 (1983). The other gene is Iml encoding myo-inositol 0-methyl transferase, derived from a stress tolerant plant (AAQ31200).
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                                                                                                                                                                                                                        T----APSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYNINETTG 142
                                                                                                                                                                                                                                                                                            92 ---LERIA-----PAIAKGOV----KRKEOGNESPLNIIACENM-VRGTTOLK-- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RQPLRKLSAGDRLIKPLL-----GTLEYGLPH 321
                                                                                                                                                                                          4 LHFGAGNIGRG----FIGKLLADA-----GIQLTFADVNQVVLDALNARHSYQVHVVGE 53
                                                                                                                                                                           29 VHFGVGNFFRAHEAFYVEQILEHAPDWAIVGVGLTGSDRSKKKAEEFKAQDC--LYSLTE 86
                                                                                                                                                                                                                                                                                                                     LGYAKARDPELAK-WIEENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLVAEDFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                370 TLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYESSEPT
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                                                                                                                                                                                                                                                                       143 AFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMSCDNLRHNGNVARKAF
                                                                                                                                                                                                                                                                                                                                                                  QWVLE-DQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SEDDPOAOELAALIADKGPOAAL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping; gene mapping; gene therapy; forension pplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                   Indels 138;
                                                                                                                              Length 382;
                                                                                                                            Query Match . 8.1%; Score 203; DB 13;
Best Local Similarity 21.3%; Pred. No. 8.9e-10;
Matches 101; Conservative 75; Mismatches 160;
                                                                                                                                                                                                                                        Claim 22; Page 47 + 36-37; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #28564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG28573 standard; Protein; 745 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 KNRIE-GIAAAMHFR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 VERVG-----
                                                                                                       382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     food supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                    203
                                                                                                                                                                                                                                                                                                                                                                  262
                                                                                                                                                                                                                                                                                                                                                                                          181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and against for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 MVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 KAPSGMTLEGYRDSVISRFSNKAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRI
                                      diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae cellular proliferation protein #524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prokaryotic cellular proliferation protein; antibacterial; drug design.
    isolated polynucleotide and encoded polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
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8.0%; Score 202.5; DB 2
Best Local Similarity 30.8%; Pred. No. 2.8e-09;
Matches 45; Conservative 30; Mismatches 70
                                                                                                                                                                                                       Claim 20; SEQ ID No 58932; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    403 AFGIASYLEMLRGRDEKGGTYESSEP 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 745 AA;
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                                                                                                                                 biodiversity
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374 ASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYESSEPTYGDA 433
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21.4%; Pred. No. 1e-08;
1ve 57; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bolotine A, Sorokine A, Renault P, Ehrlich SD;
                                                 295 ARTPIRKLG--YNERFIRPIRELKELS-----LSYKNLLK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRG ) INRA INST NAT RECH AGRONOMIQUE
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                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                ABB53324 standard; Protein; 384
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nes 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIII II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneunoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The prosent sequence represents an essent and the content of the coll proliferation in the coll proliferati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 VHFGVGNFFRAHEAFYVEQIL----EHAPDWAIVGVGLTGSDRSKKKAEEFKAQDCLYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 KAFLGYAKAR---DPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 378;
                                                                                                                                                                                                                                                                                                     Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||| || || || : : :|| || || : '| : : || || || || VHFGAGNIGRG----FIGELLFKNGFHI-DFVDVNNQIIHALNEKGKYE---
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1.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Seq ID No 13688; 511pp; English.
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                                                                                                                                                                                                                                                                                                     Zyskind JW,
                                                                      2000US-206848P
2001WO-US09180
                                                                                                                     2000US-242578P
                                                                                                                                                  2000US-253625P
                                                                                                                                                                                                 2001US-269308P
                                                                                                                                                                                                                                                                                                  Ohlsen KL,
Xu HH;
                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-611495/70.
N-PSDB; AAS55954.
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21-MAR-2001;
                                                                      23-MAY-2000;
26-MAY-2000;
                                                                                                                        23-OCT-2000;
                                                                                                                                                     27 - NOV - 2000;
                                                                                                                                                                                                 16-FEB-2001;
                                                                                                                                                                                                                                                                                                  Haselbeck R,
Yamamoto RT,
                                                                                                                                                                          22-DEC-2000;
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Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-0CT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 VHFGVGNFFRAHEAFYVEQILEHAPDWAIVGVGLTGSDRSKKKAEEFKAQDCLYSLTETA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleotide sequence useful in the identification or Lactococcus lactis and related species \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention is related to a Lactococcus lactis nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
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                                            434 EWKLAKADDFESSLKLPAFDGWRDLDTSELDQKVIVLRKIIREKGVKAAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-611495/70.
N-PSDB; AAS51999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-2000;
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                                                                                                                                                                        31
                                                                                                                                                                                                                                                                                                                               503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing a polypeptide using a cell for reducing the production of the polypeptide, comprises inserting DNA into the genome of the cell at a position not within the polypeptide coding sequence or a regulatory
| | : :||||||
----ELIKYHELIISRFSNPE 288
                                                                                                                       181 SEWVIDASHLKNK-EIKLEGVHYTTDLEPFIERKLFSVNSGHAAVAYSSAYKGYKTILEG 239
                                                                                                                                                                           -----NYLNKDVIPTLKAPSGMTLEGYRDSVISRFSNKA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus oryzae; mutant; modified; reduced transcription; hormone; reduced translation; reduced secretion; receptor; antibody; reporter; enzyme; lipase; mannitol-1-phosphate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. subtilis mannitol-1-phosphate dehydrogenase protein SEQ ID NO:28.
                                                                        HQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDA
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                                                                                                                                                                                                                            240 LODEEILNILKAVQKETRALLLAKWAQYFKQD-----
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                                                                                                                                                                                                                                                                                                             289 IIDEVSRVARTPIRKLG--YDERFIRPIRELND 319
                                                                                                                                                                                                                                                                             366 MSDQTLRIASDGCSKVQVFWTETVRRAIEDKRD 398
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96US-0713312.
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                                                                                                                                                                        321 IEDSELLGNLK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-163017/21
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13-SEP-1996;
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ABB05610
ID ABB05
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Best Local Similarity 22.5 Matches 67; Conservative

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins,
                                                 89 PSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYNINETTGAFDLEN 148
                                                                                                                           149 AAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMSCDNLRHNGNVARKAFLGYAKA 208
                                                                                                                                                           82 AALITTAVGPNVLKLIAPSIAEGLRRRNTA--NTLNIIACENMIGGSSFLKKEI--YSHL 137
                                                                                                                                                                                                   RDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLVAEDFHQWVLEDQ 268
                                                                                                                                                                                                                      Wall D, Trawick JD, Carr GJ;
             ------A 30
                                                                                   DVNETMVSLLNEKKEYTVELAE-EGRSSEIIGPVSAINSGSOTEELYRL------MNE 81
                                                                                                                                                                                                                                                                           269 FADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDAIEDSEL 326
                                                                                                                                                                                                                                                                                              of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus cellular proliferation protein #416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic cellular proliferation protein;
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LHFGAGNIGRG----FIGALLHHS------
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                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                      AAU34140 standard; Protein; 368
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2000US-207727P.
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2000US-253625P
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2001US-269308P.
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17;
and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wlpo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VHFGAGNIGRG----FIGYIL-----ADNNVKVFFADVNEEIINAL-AHDHQYDVI-LA 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.2%; Score 181; DB 22; Length 368; 21.4%; Pred. No. 8.6e-08; Live 64; Mismatches 168; Indels 132;
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Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 AA;
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Search completed: May 8, 2003, 16:32:26 Job time : 90 secs THIS PAGE BLANK (USPTO)

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APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Jensen, Richard G.
APPLICANT: Bohnert, Hans J.
TITLE OF INVENTION: Transgenic Plants With Enhanced Mannitol NUMBER OF SEQUENCES: 4
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STRET: P.O. Box 2113, First Wisconsin Plaza
CITY: Madison
STATE: W1
STATE: W1
CONNTRY: ..USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICCOSOft Word, Version #5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.0%; Score 202; DB 1; L
Best Local Similarity 20.9%; Pred. No. 2.9e-11;
Matches 99; Conservative 70; Mismatches 168;
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              US-08-465-746-2
US-08-214-164-2
US-08-246-636-2
US-08-247-491A-3
US-08-247-491A-3
US-08-247-491A-3
US-08-247-491A-3
US-08-468-985-2
US-08-469-95-2
US-08-469-434-2
US-08-214-222-2
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US-08-127-499A-23
US-08-482-847-23
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,833
                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seay, Nicholas J.
RECISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 9221490026
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/871,416
                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-186-833-2
> Sequence 2, Application US/08186833
> Patent No. 5563324
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TELEFAX: (608)251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 amino acids
                ; MOLECULE TYPE: protein US-08-186-833-2
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2516
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                GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-339-972-28
US-09-339-972-26
US-09-329-972-26
US-09-320-972-26
US-09-105-537-35
US-09-105-537-6
US-08-36-338A-10
US-08-36-338A-10
US-08-490-931-10
PCT-USS-13749-4
US-08-955-957A-2
US-08-053-614-2
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US-09-034-306-2
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Maximum Match 100%
Listing first 45 summaries
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US-08-928-692-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 LRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYESSEPTY 430
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                                                                                    PSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYNINETTGAFDLEN 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIVDKTQFKGALPNI - - PGMELTDNLMAFVERKLFTLNTGHAITAYLGKLAGHQTIRDAI 239
                                                                                                                                                                                                                                             149 AAVKADLKNPEKPSTVFGYVVEAL----RRRWDAGGKAFTVMSCDNLRHNGNVARKAFL, 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 GHVMNALPEDAKAWVEEHVGFVDSAVDRIVPP-----SASATNDPLEVTVETFSE 181
                                                                                                                                                                 ---SYQVHVVGETEQ-----VD-----VD-----TVSGVNAVSSIGD-DVVD 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SEDDPQAQELAALIADKGPQAAL 358
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APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
NUMBER OF SEQUENCES: 80
--GIQLTFADVNQVVLDALNARH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/928,692
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Patent No. 5958727
GENERAL INFORMATION:
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    4 LHFGAGNIGRG----FIGKLLADA--
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MEDIUM TYPE: Diskette
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                                                                                                                                                                         89 PSCKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYNINETTGAFDLEN 148
                                                                                                                                                                                                                                                             AAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMSCDNLRHNGNVARKAFLGYAKA 208
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                                                                                                                                                                                                                                                                                                       82 AALITTAVGPNVLKLIAPSIAEGLRRRNTA--NTLNIIACENMIGGSSFLKKEI--YSHL 137
                                                                                                                                                                                                                                                                                                                                                                          29 VHFGVGNFFRAHEAFYVEQILEHAPDWAIVGVGLTGSDRSKKKAEEFKAQDCLYSLTETA 88
                                                                                                                              ---GYDVVF----A 30
                                                                                                                                                                                                                   31 DVNETMVSLLNEKKEYTVELAE-EGRSSEIIGPVSAINSGSQTEELYRL-----MNE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                    269 FADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDAIEDSEL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
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APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
CORRESPONDENCE: 80
CORRESPONDENCE ADDRESS:
    Length 366;
                                              Indels
  Score 190; DB 2; L
Pred. No. 4e-10;
); Mismatches 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/09339972 Patent No. 6323002 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08/928,692
                                                                                                                              4 LHFGAGNIGRG----FIGALLHHS---
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    7.68; 22.58;
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COMPUTER: IBM Compatible
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REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 amino acids
                                              Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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COMPUTER READABLE FORM:
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Query Match
Best Local Similarity
Matches 67; Conserv.
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OPERATING SYSTEM:
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                                                                                                55 EEGEST--
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                                                                                                                              89 PSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYNINETTGAFDLEN 148
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                                   Gaps
                                                                                                                                                                                                                                                                                 --GYDVVF----A 30
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APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: A Polypeptide
   DB 4; Length 366;
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                                   Mismatches 121; Indels
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 Score 190; DB 4
Pred. No. 4e-10;
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APPLICATION NUMBER: US/08/978 607
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21.8%; Pred. No. 2
tive 55; Mismatch
                                                                                              4 LHFGAGNIGRG----FIGALLHHS------
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Patent No. 5958727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: LAMBLIS, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
Ouery Match 7.6%; Sc
Best Local Similarity 22.5%; Pr
Matches 67; Conservative 50;
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amino acid
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 59587
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Best Local Similarity
Matches 77; Conserva
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US-08-928-692-26
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ADDRESSEE: No. 63230020 No. 6323002disk of No. 6323002th America, Inc. STREET: 405 Lexington Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                       265 LE-DQFAD-GRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDAIE 322
                                                                                                                                                         ----KTIT--NYRAINSKTHEADVV 79
29 VHFGVGNFFRAHEAFYVEQILEHAPDWAIVGVGLTGSDRSKKKAEEFKAQDCLYSLTETA 88
                              323 DSELLGNLKNYLNK -- DVIPTLKAPSGMTLEGYRDSVISRFSNKAMSDQTLRI 373
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TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
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REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944,200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/09339972
Patent No. 6323002
GENERAL INFORMATION:
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APPLICATION NUMBER: 08/928,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yaver, Deborah
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212-867-0123
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APPLICATION NUMBER: US
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SSEQPLRLGALKSNIGHTQAAAGVAGVIKMVQAMRHGLLPKTLHVDEPSDQIDWSAGTVE 427
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Best Local Similarity 20.8%;
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                                                                                                                                                                                                                                                     QEIASADVVTCAVGPNILKFIAPVIAKGIDARTEERPVAVIACE----NAIGATDTLHGY 135
                                                                                                                                                                                                                                                                                                               LE-DOFAD-GRPPLEKAGVOMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDAIE 322
                                                                                                                                                                                                                  148 NAAVKADLKNPEKPSTVFGYVVEALRRRWDA - - GGKAFTVMSCDNLRHNGNVARKAFLGY 205
                                                                                                                                                                                                                                                                                        AKAR-DPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLVAEDFHQWV 264
                                                                                                                                               PSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYN-INETTGAFDLE 147
                                        Gaps
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                                                                      29 VHFGVGNFFRAHEAFYVEQILEHAPDWAIVGVGLTGSDRSKKKAEEFKAQDCLYSLTETA 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1562;
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: DB 4; Length 391;
2.4e-07;
 6.4%; Score 162; DB 4; Length 39
21.8%; Pred. No. 2.4e-07;
tive 55; Mismatches 149; Indels
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CURRENT APPLICATION NUMBER: US/09/320,878A

CURRENT FILING DATE: 1999-05-27

EARLIER FILING DATE: 1998-08-28

EARLIER FILING DATE: 1998-06-06

EARLIER APPLICATION NUMBER: CIP OF 09/073,538

EARLIER APPLICATION NUMBER: CIP OF 08/846,247

EARLIER FILING DATE: 1997-04-30

EARLIER FILING DATE: 1997-04-30
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EARLIER APPLICATION NUMBER: 60/100,880
EARLIER FILING DATE: 1998-09-22
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09320878A Patent No. 6117659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ASPLEY, GATY
APPLICANT: BETLACH, Welanie C.
APPLICANT: BETLACH, Mary C.
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APPLICANT: TANG, Li
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                  Best Local Similarity 21.8 Matches 77; Conservative
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Matches 100; Conserv
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LENGTH: 1562
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US-09-320-878-3
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                                                                  428 LLTEAVDWPEKQDGGLRRAAVSSFGISGTNAHVVLEEAPAVEDSPAVEPPAGGGVVPWPV 487
                                                                                                                                    DRITP-TVSAEIAKKLNAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDV 287
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SSEQPLRLGALKSNIGHTQAAAGVAGVIKMVQAMRHGLLPKTLHVDEPSDQIDWSAGTVE 427
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183 FTVMSCD-NLRHNGNVARKAFLGYAKARDP-----ELAKWIEENATF--PNG-----MV
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35
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Pred. No. 0.74;
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719 VNGPTATVVSGDPTQIEELARTCEADGVRARI-IP-----VDYASHSRQVEIIEKELA 770
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                                                                    -----RIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKG---
                                                                                                                                                     659 IAAAYVAGALTLDDAARVVTLRSKSIAAHLAGKGGMISLALDEAAVLKRLSDFDGLSVAA
                                                                                                                                                                                          ----GTYESSEPTYGDAEWKLAKADDFESSLKLPAFDGWRDLDTSELDQKVIVLRKIIR
                                                 LNKDVIPTLKA-----PSGMTLE-----GYRDSVISRFSNKAMSDQTL----
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TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600-438031
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFWARE: FastSEQ for Windows Version 3.0
SEO ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.2%; Score 105.5; DB 4;
20.8%; Pred. No. 20;
iive 74; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 TGAFDLENAAVKADLKNPEKPSTVFGYV--VEALRR-----
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09105537A Patent No. 6265202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Streptomyces venezuelae
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Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
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US-09-105-537-6
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Arginine-specific Proteinase Coding Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
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5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 LENAAVKADLK---NPEKPSTVFGYVVEA-----LRRRWDAG
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0.95;
9407 VNGPTATVVSGDPTQIEELARTCEADGVRARI-IP
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION: 430
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/119,361
FILING DATE: 10-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/265,441
FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/336,308A
FILING DATE: 08-NOV-1994
                                                                                                                                                                                                Sequence 10, Application US/08336308A
Patent No. 6017532
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
TITLE OF INVENTION: Porphyromonas gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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Best Local Similarity 21.68;
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                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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US-08-336-308A-10
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                                                                                             E 9459
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                                                      E 476
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APPLICANT: Potenpa, Jan S.
APPLICANT: Travis, James
APPLICANT: Genco, Caroline A.
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS COMPRISING
TITLE OF INVENTION: DORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                        987 HGWK-----PGNA----PGI-AGYNSNGCVYSESFGLGGIGVLTPDNYL---ITPAL 1030
                                                                                                                                                                                                                                             288 TDWEYVKIRMLNAGHVMLCFPGILVGYENVDDAIEDSELLGNL-----KNYLNKDVIPTL 342
                                                                                                                                              343 KAPSGMTLEGYRDSVISRFSNKAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRI 402
                                    928 QNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPGTTTLSESFENGIPASWKT-IDADGDG 986
229 DRIT-PTVSAEIAKKINAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDV 287
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0.95;
thes 186; Indels 114;
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APPLICATION NUMBER: US/NA/0^^
                                                                                                                                                                                                                                                                                                                     Sullivan, P.C.
                                                                                                                                                                                                                                                                                               ---FDGWRDLDTSELD 464
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21.6%; Pred. No. 0.95;
ive 60; Mismatches
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APPLICATION NUMBER: US 60/013,945
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08822324
Patent No. 6129917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Floppy disk
IBM PC compatible
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TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                               ---DDFESSL--KLPA----
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LENGTH: 1704 amino acids
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Best Local Similarity 21.6
Matches 99; Conservative
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REGISTRATION NUMBER: 3
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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987 HGWK------PGNA----PGI-AGYNSNGCVYSESFGLGGIGVLTPDNYL---ITPAL 1030
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-----GKAFTVMSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMV 228
                                                                                                                                                                                                                                                                      229 DRIT-PTVSAEIAKKLNAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDV 287
                                                                                                                                                                                                                     869 TVYRDGTKIKEGLTATTFEEDGVA-TGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPV 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Barr, Paviloff, Nadine
TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences
                                                                                                              809 FAIAAPQANAKIWIAGQGPTKEDDYVFEAGKKYHFLMKKMGSGDGTELTISEGGGSDYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 AFGIASYLEMLRGR------DEKGGT-----YESSEPTYGDAEWKLAKA----
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                                                                          --- LRRRWDAG
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Suite 201
                                                                        146 LENAAVKADLK --- NPEKPSTVFGYVVEA ---
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09490931 Patent No. 6274718 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5370 Manhattan Circle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08/336,308
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TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 24 - JUN-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : Travis, James
: Potempa, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferber, Donna M.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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US/08/955,957A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08955957A
Patent No. 6312920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Debloff, Bradley S.
APPLICANT: Rosteck Jr. Paul R.
TITLE OF INVENTION: SAM OPERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION
                                                                                                      Query Match
Best Local Similarity 19.99
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
          unknown
                                           MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Lilly CTTY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                               PCT-US95-13749-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-955-957A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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TITLE OF INVENTION: COMPOSITIONS FOR INCREASED
TITLE OF INVENTION: BIOAVAILABILITY OF ORALLY DELIVERED THERAPEUTIC AGENTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       987 HGWK------PGNA:---PGI-AGINSNGCVYSESFGLGGIGVLTPDNYL---ITPAL 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1031 DLPNGGKLTFW----VCAQDANYASEHYAVYASSTG-NDASNFTNALLEETITAK----- 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 ETAPSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYNINETTGAFD 145
                                                                                                                                                                                                                                                                            QVIPSDTHTLWPNCSVPANLFAPF -- EYTVPENADPSCSPINM - IMDGTASVNIPAGTYD 808
                                                                                                                                                                                                                                                                                                                                              928 ONLTGSAVGOKVTLKWDAPNCTPNPNPNPNPNPGTTTLSESFENGIPASWKT-IDADGDG 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 TDWEYVKIRMLNAGHVMLCFPGILVGYENVDDAIEDSELLGNL----KNYLNKDVIPTL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 KAPSGMTLEGYRDSVISRFSNKAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRI 402
                                                                                                                                                                                                                                                                                                                                                                                                 -----GKAFTVMSCDNLRHNGNVARKAFLGYAKARDPELAKWI EENATFPNGMV
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                                                                                                                                                                                                  60; Mismatches 186; Indels 114;
                                                                                                                                                               Length 1704;
                                                                                                                                                                                                                                                                                                                     146 LENAAVKADLK --- NPEKPSTVFGYVVEA -----LRRRWDAG -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLD 1176
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                                                                                                                                                               Score 105; DB 4;
Pred. No. 0.95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
      10:
                                                                                                                                                           Query Match 4.2%;
Best Local Similarity 21.6%;
Matches 99; Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 588 amino acids
amino acid
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA
                                                                                            , MOLECULE TYPE: protein US-09-490-931-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFGIASYLEMLRGR----
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                                                               amino acid
                                                                                      linear
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                                                                                 TOPOLOGY:
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PCT-US95-13749-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 ------AVLKHLVDPAIRIVSMTITEGGYNINETTGAFDL----ENAAVKADL- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 -----KNPEKPSTVFGYVVEALRRRWDAGGKAFTV-----MSCDNLRHNGNVA---- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEYVKIRM 297
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                                                                                        Gaps
                                                                                                                                                               17 PPYDIDGIKPGIVHFGVGNFFRAHEAF--YVEQ--ILEHAPDWAIVGVGLTGSDRSKKKA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----RKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKL------NAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 LDKELKAKGKSALMFNLQEPYF-TWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 FLVDLIKNKHMNADTDYSIAEA---AFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTF
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4.1%; Score 104; DB 5; Length 588;
19.9%; Pred. No. 0.21;
tive 66; Mismatches 176; Indels 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 GRDEKGGTYESSEPTYGDAEWKLAKADDFESSLKLPAFDGWRDLDTS 461
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                                                                                                                                                                                                                                           74 PQVAATGDGPDII-----FWAHDRFGGYAQSGLLAEITPDKAF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 SGLDDDLPLVAEDFHQWVLEDQFA-DGRPPLEKAGVQMVGDVTD--
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PatentIn Release #1.0, Version #1.30
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US/08/053,614

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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                               125 IVSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFT .184
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                             10 SVTEGHPD-KIADRISDTVLDALLA-RDPRARVAVETLITTGQVHIAGEVTTTAYAPIAQ
                                                                                                                                                                                                                                                                                                                                                                                                                             121 GGPGDELDROGAGDOGLMFGYACDETPELMPLPINLAHRLSRRLSEVRKNGTIPYLRPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KTQVTIEYDGDKAVRLDTVVVSSQHASGIDLD-SLLAPDIRRHVVE------PVL--AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAEDG-----IKLDTAGYRLLVNP---TGRFEIGGPMGDAGLTG-----RKIIID
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                                                                                                                                                                                                                                                                                                                                                                                                -- AKWIEENATFPNGMVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            --RITPTVSAEIAKKLNA -----ASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 IYGGMARHGGGAFSGKDPSKVDRSAAYAMRWVAKNVVAAGLASRCEVQVAYAIGKAEPVG
                                                                                                                                                                                                                                 Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE tagA GENE AND METHODS FOR DETECTING PREDISPOSITION TO PEPTIC ULCERATION
                                                                                                                                                                                                  Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 T---LKAPSGMTLEGYRDSVISRFSNKAMSDQTLRIASDGCSK-
                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                0.18;
                                                                                                                                                                                                                  ; Pred. No. 0.18 47; Mismatches
                                                                                                                                                                                                 Score 102;
                                                                                                                                                                                                                                                                83 SLTETAPSGKSTVRVMGALRDYLLAPADPEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 133 Carnegle Way, Suite 400
CITY: Atlanta
                 P-10162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08053614 Patent No. 5403924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: COVER, TIMOTHY L. APPLICANT: BLASER, MARTIN J. APPLICANT: TUMMURU, MURALI K.R.
REGISTRATION NUMBER: 39,872
           REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                 4.18; 23.18;
                                                                                                 407 amino acids
                                                                                                                                                                                                                Best Local Similarity 23.19
Matches 99; Conservative
                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 30303
COMPUTER READABLE FORM:
                                                                                                                amino acid
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TWERTDRT 398
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                                                                                                                                TOPOLOGY:
                                                                                                                                                               US-08-955-957A-2
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COUNTRY:
                                                                                                   LENGTH:
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                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 DGIEPEKVSLLYAGNGGFGAKHDWNATVGYKDQQGNNVATIINVHMKNGSGLVIAGGEKG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AFYVEQILEHAPDWAIVG---- 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VGLTGSDRSKKKAE------EFKAQD--CLYSLTETAPSGKSTVRVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423 NEIKDF---QKDSKPYLDALGNDRIAFVSKKDPKHSALITEFN-----KGDLSYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 EKPSTVFG-YVVEALRRRWDAGGKAFTVMSCDNLRHNGNVARKAFLGYAKARDPELAKWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----RITPTVSAEIAKKLNAASGLDDDLPLVAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMMURU, MURALI K.R. VENTION: THE LAGA GENE AND METHODS FOR DETECTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---LSSNKELVGKALNFNKAVAEAKNTGN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101; DB 1; L
Pred. No. 0.76;
; Mismatches 196;
                                                                                                                                                               2200.009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
                                                                       ATTORNEY/AGENT INFORMATION:
NAME: SPRATT, GWENDOLYN D.
REGISTRATION NUMBER: 36,016
                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 DGIKP --- GIVHFGVGNFFRAHE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: COVER, TIMOTHY L.
APPLICANT: BLASER, MARTIN J.
APPLICANT: HARRY KLEANTHOUS
APPLICANT: TUMMURU, MURALI K
TITLE OF INVENTION: THE tagA
                                                                                                                                                                                                                                            TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 859 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.0%;
Best Local Similarity 18.8%;
                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                               : 859 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
APPLICATION NUMBER: US
FILING DATE: 19930426
                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-053-614-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 EENATFPNGMVD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 VLRKIIREK 477
                                                   CLASSIFICATION:
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8, 2003, 16:25:50

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PREDISPOSITION TO PEPTIC ULCERATION AND GASTRIC CARCINOMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 NEIKDF---QKDSKPYLDALGNDRIAFVSKKDPKHSALITEFN-----KGDLSYT 469
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308 DGIEPEKVSLLYAGNGGFGAKHDWNATVGYKDQQGNNVATIINVHMKNGSGLVIAGGEKG 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.0%; Score 101; DB 1; Length 859; 18.8%; Pred. No. 0.76; Live 84; Mismatches 196; Indels 1
                                                                                                                                                                                           COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/316,397B
                                                                ADDRESSEE: NEEDLE & ROSENBERG, P.C. STREET: 127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2200.030
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                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SPRATT, GWENDOLYN D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 2200
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 859 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404/688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 859 amino acids
amino acid
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Best Local Similarity 18.8%
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404/688-9880
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MOLECULE TYPE: protein

US-08-316-397B-2
                                           CORRESPONDENCE ADDRESS
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                   Georgia
: USA
                                                                                                       CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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469 VLRKIIREK 477
                       775 IINQKITDK 783
                                                                                  Search completed: May
Job time : 42 secs
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58 VGVGLTGSDRSKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADPEAVLKH 117
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                                                                                                                                                                                                                                    Sequence 6
Sequence 7
Sequence 6
                                                    Sequence Seq
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                   US-09-815-242-11904
US-09-738-626-6999
US-09-738-626-6999
US-09-978-192A-526
US-09-978-192A-526
US-09-978-192A-526
US-09-978-192A-526
US-09-978-192A-526
US-10-176-758-420
US-10-176-758-420
US-10-176-738-420
US-10-174-572-420
US-10-174-572-420
US-10-174-573-420
US-10-174-573-420
US-10-174-588-420
US-10-174-588-420
US-10-174-588-420
US-10-175-738-420
US-10-175-738-420
US-10-175-738-420
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39.0%; Pred. No. 7.4e-63;
Live 82; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3626, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
GENERAL MANCAGAWA, SATOSHI
APPLICANT: MNDO, SETKO
APPLICANT: MOO, SETKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKHINO
APPLICANT: SENOH, AKHINO
APPLICANT: SENOH, AKHINO
APPLICANT: OZAKI, AKO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1900-08-03
NUMBER: DESCRIPTION NUMBER: JP 00/28098B
NUMBER: PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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US-09-738-626-3626
                                                    SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3626
LENGTH: 503
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US-09-738-626-3626
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Best Local Simi
Matches 168;
RESULT
QQ
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Sequence 6, Appli
Sequence 6, Appli
Sequence 1336, Ap
Sequence 2, Appli
Sequence 4, Appli
Sequence 11058, A
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Sequence 10385, A
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Sequence 5636, Ap
Sequence 12393, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 340, App
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Sequence 35, Appl
Sequence 35, Appl
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Sequence 3, Appli
                                                                                                                                                                                                         (without alignments)
842.122 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                        1 MITRETLKSLPANVQAPPYD.......KVIVLRKIIREKGVKAAIPA 485
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1: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISOB} \text{NEW_PUB.pep:*} \)

2: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VES_NEW_PUB.pep:*} \)

3: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \infty \) \( \text{PEDCOMB} \) \( \text{Pep:*} \)

4: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \infty \) \( \text{PEDCOMB} \) \( \text{Pep:*} \)

5: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \) \( \text{PUBCOMB} \) \( \text{Pep:*} \)

7: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \) \( \text{PUBCOMB} \) \( \text{Pep:*} \)

7: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \) \( \text{PUBCOMB} \) \( \text{Pep:*} \)

9: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \) \( \text{PUBCOMB} \) \( \text{Pep:*} \)

10: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \) \( \text{PUBCOMB} \) \( \text{Pep:*} \)

11: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \) \( \text{PUBCOMB} \) \( \text{Pep:*} \)

12: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \) \( \text{PUBCOMB} \) \( \text{Pep:*} \)

13: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \) \( \text{PUBCOMB} \) \( \text{Pep:*} \)

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13: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \) \( \text{PUBCOMB} \) \( \text{Pep:*} \)

13: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \) \( \text{PuBCOMB} \) \( \text{Pep:*} \)

14: \( \text{Cgn2} \infty \) (\text{Ptcdata} \text{1/pubpaa} \text{VISO} \) \( \text{PuBCOMB} \) \( \text{Pep:*} \)
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US-09-815-242-13688
US-09-815-242-5636
US-09-815-242-12393
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US-09-815-242-11058
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US-09-861.846-35
US-09-988-384B-35
US-09-861.289-35
US-09-861.289-6
US-09-861.289-6
US-09-98-384B-6
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US-09-824-574-3
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Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                            LEGYRDSVISRFSNKAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASY 409
                                                     LVDPAIRIVSMTITEGGYNINETTGAFDLENAAVKADLK-----NPEKPSTVFGYVVEAL 172
                                                                            173 RRRWDAGGKAFTVMSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRIT 232
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                                                                                                                                                101;
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APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA. 0111A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03:21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
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PRIOR APPLICATION WIGHER: 60/191,078
PRIOR APPLICATION WIGHER: 60/191,078
PRIOR APPLICATION WIGHER: 60/207
PRIOR FILING DATE: 2000-05-28
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-33
PRIOR APPLICATION WIGHER: 60/242,578
PRIOR APPLICATION WIGHER: 60/245,578
PRIOR APPLICATION WIGHER: 60/257
PRIOR APPLICATION WIGHER: 60/257
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-36
PRIOR FILING DATE: 2001-02-36
PRIOR FILING DATE: 2001-02-36
PRIOR FILING DATE: 2001-02-36
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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Patent No. US20020061569A1
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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89 PSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYNINETTGAFDLEN 148
                                                                                                           149 AAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKA-----FTVMSCDNLRHNGNVARKAFL 203
                                                                                                                                                                                                               204 GYAKARDPELAKWIEENA-----TFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLVA 257
                                                                                                                                                                                                                                                      A-----EEVAKYLKNPAYAEQWIGFPDAAVDRIVPLOKHE-------DPLFVQV 174
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                                                 ----IIQALKERKSYTIELADAS-----HQQINVENVT-----GLNNMTEPEKVVE 77
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
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5.4e-10;
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21.9%; Pred. No. 5.4e
tive 71; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-12-22
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Trawick, John D.
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US-09-815-242-10385
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                                                                                                                                      143 AFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMSCDNLRHNGNVARKAF 202
                                                                                                                                                                              89 PVVLERIA-----PAIAKGOV----KRKEQGNESPLNIIACENM-VRGTTQLK-- 131
                                                                                                                                                                                                                    203 LGYAKARDPELAK-WIEENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLVAEDFH 261
                                                                                                                                                                                                                                             QWVLE-DQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDA 320
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4 LHFGAGNIGRG----FIGKLLADA-----GIQLTFADVNQVVLDALNARHSYQVHVVGE
                                                                                                                                                                                                                                                                                                                                        181 EWIVDKTQFKGALPNI--PGMELTDNLMAFVERKLFTLNTGHAITAYLGKLAGHQTIRDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 TLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYESSEPT
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APPLICANT: Yamamoto, Robert T.
APPLICANT: XU, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
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Patent No. USZ0020061569Al
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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-09-815-242-13688
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DB 10; Length 378;

7.9%; Score 200;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 AEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYEN 316
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                                          Gaps
                                                                                                 29 VHFGVGNFFRAHEAFYVEQIL----EHAPDWAIVGVGLTGSDRSKKKAEEFKAQDCLYSL 84
                                   Mismatches 163; Indels 130;
                                                                                                                                                                                                                                                                                    49 IEIAQKGQSRIEVTNVAG--INSKEHPEQVIE----AIQKTDIITTAIGPNI---
                                                                                                                                        5 VHFGAGNIGRG----FIGEILFKNGFHI-DFVDVNNQIIHALNEKGKYE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-12

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-10-25
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SOFTWARE: FastSEQ for Windows Version 4.0
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Yamamoto, Robert T.
   22.6%;
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Zyskind, Judith W.
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TOTATANT: Trawlick, John D.
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APPLICANT: Haselbeck, Robert
Best Local Similarity 22.69
Matches 106; Conservative
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US-09-815-242-5636
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TYPE: PRT
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89 PSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYNINETTGAFDLEN 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 FADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDAIEDSELLG 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 ---DITGPLGHNIHFANSAVDRIVPLQKNE------NILDVMVEPFYEWVVEKD 177
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                                                                                                                                                                                                                                                                                          4 VHFGAGNIGRG----FIGYIL-----ADNNVKVTFADVNEEIINAL-AHDHQYDVI-LA
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21.2%; Pred. No. 0.052;
ive 65; Mismatches 165; Indels 148;
                                                                                                                                                              Length 368;
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US-09-932-145-7
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APPLICANT: Feder, John N.
APPLICANT: Mintier, Gabe
APPLICANT: Ramanathan, Chandra S
TILLE OF INVENTION: NOVEL IMIDAZOLINE RECEPTOR HOMOLOGS
FILE REFERENCE: D0020 NP
CURRENT FPLICATION NUMBER: US/09/932,145
CURRENT FILING DATE: 2001-08-17
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                                                                                                                                                              7.2%; Score 181; DB 10;
21.4%; Pred. No. 7e-08;
                                                                                                                                                                                                               168;
                                                                                                                                                                                                               Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12393
LENGTH: 368
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                                                                                                                                                                                                               64;
                                                                                            ; ORGANISM: Staphylococcus aureus US-09-815-242-12393
                                                                                                                                                                                                               Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 102; Conserv
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Best Local Similarity
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                                                                      TYPE: PRT
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                                                                                                                    Gaps
                                                                                                                                                              29 VHFGVGNFFRAHEAFYVEQILEHAPDWAIVGVGLTGSDRSKKKAEEFKAQDCLYSLTETA 88
                                                                                                                                                                                                            4 VHFGAGNIGRG----FIGYIL-----ADNNVKVTFADVNEEIINAL-AHDHQYDVI-LA 51
                                                                                                                                                                                                                                                                                                           ----NNVDA-----INSMQPSEALKQ
                                                                                                                                                                                                                                                                                                                                                                                    NLKNYLNKDVIPTLKAPSGMTLE------GYRDSVISRFSNKAMSDQTLRIASDGCS
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                                                                                                                  Indels 132;
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                                                                 ; Score 181; DB 10; I; Pred. No. 7e-08; 64; Mismatches 168;
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PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-11-27
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; ORGANISM: Staphylococcus aureus US-09-815-242-5636
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Yamamoto, Robert T
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Wall, Daniel
Trawick, John D.
                                                                 ch 7.2%;
1 Similarity 21.4%;
99; Conservative 6
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APPLICANT: Haselbeck, Robert
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                                                                                            Best Local Similarity
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US-09-815-242-12393
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is for Improving Secondary Metabolite Production in Fungi
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                                                                  ODAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVIS 359
                                                                                      DGCSKVQVFWTETVRRAIEDKRDLSRIAFG---IASYLEMLR 414
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------RQDKKN-KRLKFGHRLIATHTNLER 642
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EDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLN 299
                   SEFARRROPTDQ-NNQSNLNGGNNTQQPGTNSHYNNTNTDNV 338
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.5%; Pred. No. 2.5;
e 75; Mismatches 168; Indels 114; Gaps
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-RLQALKANDEEAYIKL 670
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TDWEYVKIRM----
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Matches 100; Conserv
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US-09-861-289-35
                      476 E 476
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                                                                                                                                          659 IAAAYVAGALTLDDAARVVTLRSKSIAAHLAGKGGMISLALDEAAVLKRLSDFDGLSVAA 718
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                                      300 AGHVMLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVIS 359
                                                                            562 NTH-----PNFLSKIRNIN--VQDALLTNQL--YKNHEL------LKLERKKTEAVA 603
                                                                                                                  RFS..NKAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFG---IASYLEMLR 414
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505 LOTTVNDCLDKLLNDECTESTRENALYDYYALQLLPLQKA---VRGHVLQFEWHQNSLLT 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILLE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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SOFTWARE: FastSEQ for Windows Version 3.0
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; ORGANISM: Streptomyces venezuelae
US-09-860-846-35
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                                                                                                                                                      604 RLKSMNKSAINOYNR-
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Llarity 20.8%; Pred. No. 2.9;
Conservative 74; Mismatches 194;
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                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/988,384B CURRENT FILING DATE: 2001-11-19 PRIOR APPLICATION NUMBER: PCT/US99/14398 PRIOR FILING DATE: 1999-06-25 PRIOR APPLICATION NUMBER: US 09/105,537 PRIOR FILING DATE: 1998-06-26
Sequence 35, Application US/09988384B publication No. US20030073824A1. GENERAL INFORMATION: APPLICANT: Sherman, D.H.
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SEQ ID NO 35
LENGTH: 1562
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LENGTH: 11877
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                                                                                                                    TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR PLICH DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35
LENGTH: 1562
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20.8%; Pred. No. 2.9;
tive 74; Mismatches
Sequence 35, Application US/09861289 Patent No. US20020110897A1
                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptomyces venezuelae US-09-861-289-35
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Patent No. US20020164742A1
                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity 20.8
100; Conservative
                                                       APPLICANT: Sherman, D.H.
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                                                                                                           Zhao, L.
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APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
                                                                          Liu, H.
Xue, Y.
                                    GENERAL INFORMATION:
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US-09-860-846-6
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PAPLICANT: Zhao, L.
TILLE OF INVENTON: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
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20.8%; Pred. No. 57;
*ive 74; Mismatches 194;
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CURRENT APPLICATION NUMBER: US/09/860,846
                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 6
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CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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SOFTWARE: FastSEQ for Windows Version 3.0
                    CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION UNMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
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, Sequence 6, Application US/09861289
; Patent No. US20020110897A1
; GENERAL INFORMATION:
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US-09-860-846-6
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Search completed: May
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                                                                                                               Length 11877;
                                                                                                4.2%; Score 105.5,
20.8%; Pred. No. 57;
+ive 74; Mismatches 194; Indels 113;
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Pred. No. 59;
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CURRENT APPLICATION NUMBER: US/09/988,384B
CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,537
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; ORGANISM: Streptomyces venezuelae
US-09-861-289-6
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GENERAL INFORMATION:
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SEQ ID NO 6
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                                                                                                            Query Match
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US-09-988-384B-6
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87 TAPSGKSTVRVM-GALRDYLLAPADPEAVLKH-----LVDPAIRIVSMTITEGGYNINET 140

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8, 2003, 16:31:27

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9729 VNGPTATVVSGDPTQIEELARTCEADGVRARI-IP------VDYASHSRQVEIIEKELA 9780
9669 IAAAYVAGALTLDDAARVVTLRSKSIAAHLAGKGGMISLALDEAAVLKRLSDFDGLSVAA 9728
                                                                                                                                                                                                                                                                                                                                                                                                               TDWEYVKIRM------LNAGHVMLCFPG----ILVGYENVDDAIEDSELLGNLKNY 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNKDVIPTLKA----PSGMTLE-----371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GTYESSEPTYGDAEWKLAKADDFESSLKLPAFDGWRDLDTSELDQKVIVLRKIIR 475
                                                                                                                                                                                            183 FIVMSCD-NLRHNGNVARKAFLGYAKARDP-----ELAKWIEENATF--PNG-----MV
                                                                                                                                                                                                                                              9438 LLTEAVDWPEKQDGGLRRAAVSSFGISGTNAHVVLEEAPAVEDSPAVEPPAGGGVVPWPV
                                                                                                                                                                                                                                                                                                    DRITP-TVSAEIAKKLNAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKG---
                                                                                    TGAFDLENAAVKADLKNPEKPSTVFGYV - - VEALRR - .
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                   OM protein - protein search, using sw model
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                                                                                                                             Run on:
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8, 2003, 16:29:57 ; Search time 46 Seconds
(without alignments)
1013.591 Million cell updates/sec US-09-926-163B-2 2516 1 MITRETLKSLPANVQAPPYD.......KVIVLRKIIREKGVKAAIPA 485 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_73:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mannitol dehydroge	.~	probable fructuron	D-mannonate oxidor	mannonate oxidored	fructuronate reduc	probable fructuron		mannitol 2-dehydro	probable oxidoredu	fructuronate reduc	probable D-mannona	probable oxidoredu	probable oxidoredu	probable fructuron		mannitol 2-dehydro	mannitol 2-dehydro	mannitol 2-dehydro	fructuronate reduc	mannitol dehydroge	mannitol dehydroge	probable mannitol	hypothetical prote	fructuronate reduc	altronate oxidored	probable tagaturon	altronate oxidored	tagaturonate reduc
SUMMARIES	ID	D83353	S50519	A96022	B91289	E86130	S56548	A64909	G90897	T03548	Н85719	AD0679	AF0156	н91011	B85856	C64986	AH0883	AG3103	C98183	F87433	AE3569	A99293	AH2990	AF0283	H72422	н86828	E96985	C69853	D83711	AB0072
	DB	7	7	7	~	7	~	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
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фP	Query	36.6	31.4	31.0	30.8	30.8	30.8						29.9	29.7	29.7	29.4	29.0	29.0	29.0	28.7			25.9				13.7.	13.2	11.9	11.4
	Score	922	789	179	775.5	775.5	774.5	771.5	769.5	768	763.5	759.5	753.5	746.5	746.5	739.5	730	730	730	721	700.5	650.5	650.5	569	371	365.5	343.5	331	299.5	288
	Result No.	-	7	e	4	ស	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

altronate oxidored	attionate oxidored		propante signa rac	mannitol-1-phospha	mannitol-1-phospha	mannitol-1-phospha	mannitol-1-phospha	mannitol-1-phospha	hypothetical prote	mannitol-1-phospha	mannitol-1-phospha	mannitol-1-phospha	mannitol-1-phospha	mannitol-1-phospha
H90894	A03/23	D04906	D31188	D86035	B65160	AE0494	C39435	C44798	Н86627	139888	G97916	H95045	C90011	AH0976
7 7	4 C	N C	ا د	2	~	7	7	7	7	7	7	7	7	7
483	0 0 0	204	7 00	382	382	387	374	382	385	366	378	378	368	382
11.3	1001	70.0	, œ	8 .2	8.1	8.0	7.7	7.6	7.6	7.6	7.6	7.5	7.4	7.4
285	27.5	2,000	206	206	205	202.5	193	192	191.5	190	190	188	186	185

ALIGNMENTS

RESULT 1 D83353 mannitol dehydrogenase PA2342 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Decies: Pseudomonas aeruginosa C;Decies: Pseudomonas aeruginosa C;Decies: Decies: Decient Sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Dete: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Dete: 15-Sep-2000 C;Decies: Decient Sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: D83353 A;Cture 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID: 20437337; PMID: 10984043 A;Recession: D83353 A;Status: preliminary A;Rolecule type: DNA A;Recession: D8353 A;Status: preliminary A;Rolecule type: DNA A;Recession: D8353 A;Status: preliminary A;Rolecule type: DNA A;Recession: D8342 A;Cross references: GB:AE004660; GB:AE004091; NID:99948372; PIDN: AAG05730.1; GSPDB:GN A;Experimental source: strain PA01 C;Gene: mtlD; PA2342 C;Gene: mtlD; PA2342	Ouery Match 36.6%; Score 922; DB 2; Length 491; Best Local Similarity 45.2%; Pred. No. 3.3e-57; Matches 199; Conservative 66; Mismatches 171; Indels 4; Gaps 2; 2 ITRETLKSLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQILEHAPDWAIVG 59	: 1:	DPAIRIVSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAG 179	240 AKKLNAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLN 299 	300 AGHVMLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVIS 359 :	360 RFSNKAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEK 419 + -
RESULT 1 D83353 mannitol de mannitol de C, Date: 15- C, Date: 15- C, Accession R, Stover, S. Adman, S.; Adman,	ery Mi st Loc tches	3 63	120 121 180 181	240	300	360
RESULT D83353 Manic C, Spec C, Date C, Date C, Date C, Date M, Stone A, Refe A, Acce A, Acce A, Statt A, Mole A, Stone C, Gene C, C, Gene C, C, Gene C, C, C	Ouc Bes Ma	oy oy	oy Oy	Qy	Oy Dp	Qy

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Assetus: preliminary
Associates: DNA
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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001
C;Dates: 20-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001
C;Accession: A96022
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; He
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Tille: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing of A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable fructuronate reductase (EC 1.1.1.57) [imported] - Sinorhizobium meliloti
                                                                                                                                                                ||| :| :| |||||||||| :| CLINE || : ::|:: |: || || || || :: : VGLMKADALMRDA--MKAQDCLYTLVERGIK-DTNAYIVGSITAYMYAPDDPRAVIEKMA 128
                                                                                                                                                                                                                                                                 DPAIRIVSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                              180 GKAFTVMSCDNLRHNGNVARKAFLGYAK-ARDPELAKWIEENATFPNGMVDRITPTVSAE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAGHVMLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRFSNKAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRD--LSRIAFGIASYLEMLRGR 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEKGGTYESSEPTYGDAEWKLAKADDFESSLKLPAFDGWRD-----LDTSEL-DQK 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---MAPTLKAAAVKGGKDPHELLNIEVLFSPEIRDNK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERFSNPAIQDIVARICLMGSGKMPKYVLPSIYEQLR-KPDGKYKLLAVCVAGWFRYLIGV 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ITRETLKSLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQILEHAPDWAIVGVG 61
239 IAKKLNAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 31.0%; Score 779; DB 2; I Best Local Similarity 38.9%; Pred. No. 3.9e-47; Matches 166; Conservative 77; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Genome: plasmid
C;Superfamily: conserved hypothetical protein YEL070w
C;Keywords: oxidoreductase
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                                                                                                                9
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                                                                                                                                                                                                                                                                                     RESULT 2
Sportbettcal protein VELO7Ow - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein N3810; hypothetical protein VNR073c
C;Species; Saccharomyces cerevisiae
C; Species; Saccharomyces cerevisiae
C; Date: 2B -May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001
C; Accession: $50519; $563406; $53411; $54055; $53890
R; Dietrich, F.S.
submitted to the DMBL Data Library, December 1994
A; Description: The sequence of S. cerevisiae cosmids 9669, 8334, 8199, and lambda clone
A; Reference number: $50434
A; Residues: 1-502 Anna
A; Residues: 1-502 Anna
A; Reference number: $63010
A; Accession: $63010
A; Reference number: $63020
A; Reference number: $63020
A; Reference number: $63020
A; Reference number: $63040
A; Referen
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    361 RFANRAIADQLERVCSDGSSKFPKFIVPTANRLIAAGRPLERVALVVAAWALYLGGVDEH 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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A;Title: Sequencing of a 9.2 kb telomeric fragment from the right arm of A;Reference number: $63890; MUID:97060021; PMID:8904342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
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;Levesque, H.; Lepingle, A.; Nicaud, J.M.; Gaillardin, C.
east 12, 289-295, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 8e-48;
90; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Map position: 14R Superfamily: conserved hypothetical protein YEL070w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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Pred. No. 6
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                                                                            420. GGTYESSEPTYGDAEWKLAK 439
                                                                                                                                                    GERYPIPDPRAAECQALVAE 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.48;
35.78;
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Cross-references: EMBL:X86790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:X86790
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Best Local Similarity 35.7
Matches 179; Conservative
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C; Genetics : <<11
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ITRETLKSLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQILE--HAPDWAIVG 59

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Db 243 QLGVYDPCAIACEPFRQWYIEDNEVVGRPUNDVVPERMKLRMLNGSHSFL 302 Qy 306 CPPGILVGYERVDDAIEDSELLGALKNYLNKDVIPTILRAPSGWILEGYBRDSVLSRENKA 365 ii	A.Cross-references: GB:AR005174; NID;91251933; PIDN:AAG59565.1; GSPDB:GN00145; UWGP: A.Experimental source: strain 0157:H7, substrain ED1933 C; Genetics: A.Gene: uxuB C; Genetics: A.Gene: uxuB C; Superfamily: conserved hypothetical protein YEL070w Ouery Match Ouery Matc
Db 3 LSRKTIDRLEPRTVKRPHYDLGTVTVGIVHLGIGAFHRAHQAVTDGLLSEDPSWGICGVS 62 Qy 122 LTGSDRSKKKAEEFKAQDCLYSLTETAPSGKSTVWVGALROLAPDDPEAVLRHUVDP 121 1 1 1 1 1 1 1 1 1	C:Dete: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. Na: 86. 11-22, 2001 A:Jil-12. 3001

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A; Molecule type: DNA
A; Residues: 1.486 <BLAT>
A; Cross_references: GB:AE000251; GB:U00096; NID:g1787814; PIDN:AAC74615.1; PID:g17878
A; Experimental source: strain K-12, substrain M01655
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: reversible reaction of D-mannonate and NAD(+) to D-fructuronate and NA A; Pathway: D-glucuronate catabolism A; Note: part of the interconversion of D-fructuronate to D-2-keto-3-deoxy-D-gluconate A; Note: reduces also D-tagaturonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC 1.1.1.57) ydfI - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N'Alternate names: D-mannonate oxidoreductase
C;Species: Escherichia coli
C;Species: Escherichia coli Mar-2002
C;Species: D-my Mau, B; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                  SEPTYGDAEWKLAKADDFESSLKLPAFDGWRDLDTSELDQK-----VIVLRKIIREKGV 479
                                                                                                                                                                                    CDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAAS 247
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303 AYLGYLGGYETIADTVTNPAYRKAAFALMMQEQAPTLSMPEGTDLNAYATLLIERFSNPS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADP-EAVLKHLVDPAIRIVS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRWDAGGKAFTVMS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQI-LEHAPDWAIVGVGLTGSDRS 68
                                                  MSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYES
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C;Superfamily: conserved hypothetical protein YEL070w
C;Keywords: carbon-oxygen lyase; hydro-lyase; NAD; oxidoreductase
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C;Function:
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A; Cross-references: EMBL:014003; NID:g1263172; PIDN:AAA97219.1; PID:g537164
A; Cross-references: EMBL:014003; NID:g1263172; PIDN:AAA97219.1; PID:g537164
B; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Recession: E65246
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Restences: GB:AE000503; GB:U00096; NID:g1790777; PIDN:AAC77279.1; PID:g1790779;
A; Experimental source: strain K-12, substrain MG1655
C; Genetics:
A; Gene: usub
C; Function:
A; Description: reversible reaction of D-mannonate and NAD(+) to D-fructuronate and NADH
A; Pathway: D-glucuronate catabolism
A; Note: part of the interconversion of D-fructuronate to D-2-keto-3-deoxy-D-gluconate
A; Note: reduces also D-tagaturonate
C; Superfamily: conserved hypothetical protein YEL070w
C; Keywords: carbon-oxygen lyase; hydro-lyase; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                      Nalternate names: D-mannonate oxidoreductase
C;Species: Bscharichia coli
C;Species: Bscharichia coli
C;Accession: 356548; E65246
R;Burland, V.; Plunkett III., G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A;Reference number: S56314; MUID:95334362; PMID:7610040
A;Accession: S56548
A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNA 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTV 185
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  --- VIVLRKIIREKGV 479
                                               423 VDPML--AEFOKINA-OYOGADRVKALLGLSGIFADDLPQNADFVGAVTAAYQOLCERGA 479
                                                                                                                                                                                                                                                                                   fructuronate reductase (EC 1.1.1.57) uxuB - Escherichia coli (strain K-12)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 NLP--VARPSWDHSRLESRIVHLGCGAFHRAHQALYTHHLLESTDSDWGICEVNLMPGND 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.8%; Score 774.5; DB 2;
36.4%; Pred. No. 8e-47;
iive 86; Mismatches 206;
426 SEPTYGDAEWKLAKADDFESSLKLPAFDGWRDLDTSELDQK--
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Best Local Similarity 36.4%;
Matches 177; Conservative
                                                                                                    480 KAAIPA 485
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K.; Apoda
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C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                 Rhodobacter capsulatus SB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF010496; NID:93128256; PIDN:AAC16201.1; PID:93128349
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Potamousis,
                                                                                                                           C;Accession: T03548
R;Vicek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M. Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter caps: A;Reference number: 214955; MUID:97404404; PMID:9256491
A;Accession: T03548
                                                         mannitol 2-dehydrogenase - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |: || :: | :: | :: | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
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R;Perna, N.T; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 478;
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Best Local Similarity 36.4%; Pred. No. 2.2e-46;
Matches 176; Conservative 84; Mismatches 202;
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C;Superfamily: conserved hypothetical protein YEL070w
                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-478 <VLC>
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                                                                                                                                                                                                                                                                                                                                                               probable oxidoreductase ECs2151 [imported] - Escherichia coli (strain 0157:H7, substrain C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Bs. 18-11-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C; Accession: G90897 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B, 11-22, 2001 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc A; Reference number: A99629; MUID:21156231; PMID:11258796 A; Accession: G90897 A; Accession: G90897 A; Accession: G90897 A; Residues: I-486 c.Hay> A; Molecule type: DNA A; Residues: I-486 c.Hay> A; Cross-references: GB:BA000007; PIDN:BAB35574.1; PID:g13361617; GSPDB:GN00154 A; Experimental source: strain 0157:H7, substrain RIMD 0509952 A; Gene: ECs2151 C; Superfamily: conserved hypothetical protein YEL070w
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                                                                                             KKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADP-EAVLKHLVDPAIRIVS 127
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probable D-mannonate oxidoreductase YPO1280 [imported] - Yersinia pestis (strain C092 C; Species: Yersinia pestis
C; Species: Versinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C; Accession: AF0156
R; Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G il, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNMPENGHVTRQVVTAYAREVDAELAIMIEQNVTPPSTMVDRIVPAVTPETLDKIEQLT 241
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                                                                                                                                                                                                                                                                                                 KKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADP-EAVLKHLVDPAIRIVS 127
                                                                                                                                                  10 LPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQI-LEHAPDWAIVGVGLTGSDRS
                                                                                                                                                                                             MIITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87; Mismatches
Score 759.5;
Pred. No. 9.2
30.2%; 3
                                      Best_Local Similarity 36.39
Matches 175; Conservative
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A;Molecule type: DNA
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SV 480
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       Query Match
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; PMID:11677608
A;Accession: Ab0679
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AL513382; PIDN:CAD01805.1; PID:g16502650; GSPDB:GN00176
C;Genetics: STAL53
C;Superfamily: conserved hypothetical protein YEL070w
C;Keywords: oxidoreductase
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-486 <STDO.
A; Residues: 1-486 <STDO.
A; Cross-references: GB:AE005174; NID:g12515111; PIDN:AAG56220.1; GSPDB:GN00145; UWGP:Z21
A; Experimental source: strain 0157:H7, substrain EDL933
C; Genetics:
A; Gene: yoff
C; Superfamily: conserved hypothetical protein YEL070w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 PGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRFSNKAMS 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADP-EAVLKHLVDPAIRIVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LPANVQAPPYDIDGIKPGIVHFCVGNFFRAHEAFYVEQI-LEHAPDWAIVGVGLTGSDRS
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                                                                                                                                                                                                                                                                                                 Length 486;
                                                                                                                                                                                                                                                                                                 30.3%; Score 763.5; DB 2; 37.7%; Pred. No. 4.8e-46; ive 78; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 37.7
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                       Similarity
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9
A, Cross-references: GB: AL590842; PIDN: CAC90113.1; PID: 915979333; GSPDB: GN00175
                                                                                                                                                                                                                                          SKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADP-EAVLKHLVDPAIRIV 126
                                                                                                                                                                                                                                                               SLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQILE-HAPDWAIVGVGLTGSDR
                                                                                                                                                                                        Length 490;
                                                                                                                              Indels
                                                                                        29.9%; Score 753.5; DB 2;
llarity 37.8%; Pred. No. 2.4e-45;
Conservative 80; Mismatches 190;
                                      A;Gene: YPO1280
C;Superfamily: conserved hypothetical protein YEL070w
                                                                                                             Similarity
                                                                                                             Best Local Sim
Matches 171;
                                                                                              Query Match
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probable oxidoreductase yelQ [Imported] - Escherichia coli (strain O157:H7, substrain Cispecias: Escherichia coli (Scherichia coli Cispecias: Escherichia coli Cispecias: Escherichia coli Cispecias: 16 Feb-2001 #sequence_revision 16 Feb-2001 #text_change 14-Sep-2001 Cisacession: B65856 Figura N. T.; Plunkett III. G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May Ripera N. T.; Plunkett III. G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May Nature 409, 529-533, 2001 Figura N. T.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005174; NID:g12516498; PIDN:AAG57310.1; GSPDB:GN00145; UWGP: A;Experimental source: strain 0157:H7, substrain EDL933
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                                                           SDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYESS 426
                                                                                             :| :| | | | | : : | | | | : : | | : | 363 KHKTWQIAMDGSQKLPQRMLAGIRIHLGRETDWSLLALGVAGWMRYVSGVDDAGNAIDVR 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAA 246
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C;Superfamily: conserved hypothetical protein YEL070w
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DP 424
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                                                       SMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVM 186
                                                                                                                                        SCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAA 246
                                                                                                                                                                                                                                                           SGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLC 306
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29.7%; Score 746.5; DB 2;
Best Local Similarity 37.7%; Pred. No. 7.6e-45;
Matches 159; Conservative 81; Mismatches 175;
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Escherichia coli

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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                               A; Gene: yeio

C; Function:

A; Description: reversible reaction of D-mannonate and NAD(+) to D-fructuronate and NADH

A; Pathway: D-glucuronate catabolism

A; Note: part of the interconversion of D-fructuronate to D-2-keto-3-deoxy-D-gluconate

A; Note: reduces also D-tagaturonate

C; Superfamily: conserved hypothetical protein YEL070w

C; Reywords: carbon-oxygen lyase; hydro-lyase; NAD; oxidoreductase
                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-488 <BLAT>
A; Cross-references: GB:AE000306; GB:U00096; NID:g1788489; PIDN:AAC75233.1; PID:g1788497;
A; Experimental source: strain K-12, substrain MG1655
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1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
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                                                                                                                                                                       A;Accession: C64986
A;Status: nucleic acid sequence not shown; translation not shown
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37.7%;
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Best Local Similarity 37.7
Matches 159; Conservative
                       C;Accession: C64986
R;Blattner, F.R.; Pl
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8, 2003, 16:34:29

Search completed: May Job time: 47 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein 8, 2003, 16:25:56; Search time 27 Seconds Мау Run on:

(without alignments)
745.038 Million cell updates/sec

US-09-926-163B-2 2516

1 MITRETLKSLPANVQAPPYD........KVIVLRKIIREKGVKAAIPA 485 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 Total number of hits satisfying chosen parameters:

112892 segs, 41476328 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description .	9941 saccl	0916	P77260 escherichia	P33029 escherichia				O52720 klebsiella	Q47826 erwinia her					Q45421 bacillus st	P27543 enterococcu				Q9xbm6 klebsiella	P57634 buchnera ap	P80868 bacillus su	P11532 homo sapien	P11531 mus musculu			bacill	097592 canis famil	P22082 saccharomyc	. P44669 haemophilus	_	SS	2331	Q98qd8 mycoplasma
SUMMARIES	QI	YEIO_YEAST	UXUB_ECOLI	YDFI_ECOLI	YEIQ_ECOLI	MTLK_RHOSH	DALD_RALSO	DALD_YERPE	DALD_KLEPN	YTUB_ERWHE	UXAB_ECOLI	POR_GLUOX	MTLD_CLOAB	MTLD_ECOLI	MTLD_BACST	MTLD_ENTFA	MTLD_STRMU	MTLD_BACSU	MTLD_BACHD	MTLD_KLEPN	MTLD_BUCAI	EFG_BACSU	DMD_HUMAN	DMD_MOUSE	RPC_BPPHC	RRP1_INCJJ	EFG_BACHD	DMD_CANFA	SNF2_YEAST	HSCA_HAEIN	YTX1_XENLA	FTZ1_PYRAB	VPS5_YEAST	EFG_MYCPU
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Q9cds1 lactococcus	P12882 homo sapien	Q9y623 homo sapien	Q9ukx2 homo sapien	Q8tmt1 methanosarc	P20735 sus scrofa	P43299 arabidopsis	O9xdh6 pseudomonas	P36541 escherichia	Q10478 schizosacch	Q8zim7 yersinia pe
DPO1_LACLA	MYH1_HUMAN	MYH4_HUMAN	MYH2_HUMAN	DNL1_METAC	GGT_PIG	PROL_ARATH	DP3A_PSEFL	HSCA_ECOLI	YDF6_SCHPO	DNAK_YERPE
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103	103	103	103	102	101	101	101	100.5	100	100

ALIGNMENTS

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                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (YEL070W).

STRAIN=S288C / AB972;

Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelcon M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                      (Rel. 31, Last Sequence update)
(Rel. 40, Last annotation update)
1 56.5 kDa protein in HXT8 5'region and in HXT17-COS10
                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceteles;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Levesque H., Nicaud J.-M., Lepingle A., Gaillardin C.; "Sequencing of a 9.2 kb telomeric fragment from the right arm of Saccharomyces cerevisiae chromosome XIV."; Past 12:289-295(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A. (YNR073C).
Andre B., Iraqui Houssaini I., Urrestarazu L.A., Vissers S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                       AA.
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STRAIN=S288c;
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EMBL; 271688; CAA96356.1; -.
EMBL; 271689; CAA96358.1; -.
EMBL; X86790; CAA60486.1; -.
SGD; S0000796; YEL070W.
SGD; S0005356; YRR073C.
InterPro: IPR000669; Mannitol_dh.
Pfam; PF01223; Mannitol_dh; I.
PRINTS; PR00084; MILDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97060021; PubMed=8904342;
                                                                                                                                                                    YEL070W AND (YNR073C OR N3810).
                                                                          31, Created)
                                     .STANDARD;
                                                                          (Rel.
                                                                                                                                                     intergenic region.
                                                                    01-FEB-1995 (
01-FEB-1995 (
16-OCT-2001 (
                                                                                                                                 Hypothetical
                                   YEIO_YEAST
P39941;
RESULT 1
YEIO_YEAST
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Query Match
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                                                                                                                                            Gaps
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Submitted (SEP-1992) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-mannonate + NAD(+) = D-fructuronate + NADH
                                                                                                                                                                                        2 ITRETLKSLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQILE--HAPDWAIVG 59
                                                                                                                                                                                                                     DPAIRIVSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAG
                                                                                                                                                                                                                                                                                                                                                                                                         GKAFTVMSCDNLRHNGNVARKAFLGYAK - ARDPELAKWIEENATFPNGMVDRITPTVSAE
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16-OCT-2001 (Rel. 40, Last annotation update)
D-mannonate oxidoreductase (EC 1.1.1.57) (Fructuronate reductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAKKLNAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRML
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
Blattner F.R.;
"Analysis of the Escherichia coli genome VI: DNA sequence of
region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
                                                                                           Length 502;
                                                                                                                                         Indels
                      l protein; Oxidoreductase; NAD.
502 Aa; 56470 MW; A7E0CC01AADC1B2A CRC64;
                                                                                           31.4%; Score 789; DB 1; Le
35.7%; Pred. No. 1.3e-46;
tive 90; Mismatches 195;
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PROSITE; PS00974; MANNITOL_DHGENASE; 1.
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01-FEB-1995 (Rel. 31, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                         Matches 179; Conservative
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                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 MSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 LRHRTWQIAMDGSQKLPQRLLDPVRLHLQNGGSWRHLALGVAGWMRYTQGVDEQGNAIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYES
SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 486;
                                                                                                                                                                                                                                                                       EMBL; U14003; AAA97219.1, -..
EMBL; D13229; BAA02591.1; -..
R EMBL; D1329; BAA02591.1; -..
R ECGENE; EG20248; uxuB.
R InterPro; IPR000669; Mannitol_dh.
R Pfam; PF010232; Mannitol_dh.
R PRINTS; PR00084; MTLDHDRGNASE, 1...
DR PROSTTE; PS00974; MANNITOL_DHGENASE; 1...
DR PROSTTE; PS00974; MANNITOL_DHGENASE; 1...
NP BIND ... 53580 MW; 7835638682AF7B87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2e-45;
ches 206;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OGT-2001 (Rel. 40, Last annotation update)
19pothetical oxidoreductase ydfI (EC 1----).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.8%; Score 774.5;
36.4%; Pred. No. 1.2e
iive 86; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 36.4 Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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P77260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADP-EAVLKHLVDPAIRIVS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QQIADLQQQDNLYTVAEMS-ADVWTARVVGVVKKALHVQIDGLETVLAAMCEPQIAIVS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRWDAGGKAFTVMS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQI-LEHAPDWAIVGVGLTGSDRS 68
                                                                                               MEDLINE-97426617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMYGDVTDWEYVKIRMLNAGHVMLCF
                                                                                                                                                                                                                                                                                                          Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasal H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Salto N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 3:363-377(1996).
-!- SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Oxidoreductase; NAD; Complete proteome. NP_BIND 24 35 NAD (BY SIMILARITY). SEQUENCE 486 AA; 53685 MW; 96F3BF07AE114B70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           "A 570-kb DNA sequence of the Escherichia coli K-12 genome
                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.7%; Score 771.5; DB 1; ilarity 37.7%; Pred. No. 1.9e-45; Conservative 81; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00974; MANNITOL_DHGENASE; 1.
                                                                                                                                                                                                                                                                                           MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000669; Mannitol_dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000251; AAC74615.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01232; Mannitol_dh; 1.
PRINTS; PR00084; MTLDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, D90797; BAA15243.1; -. EMBL, D90798; BAA15247.1; -. EcoGene; EG13821; ydfI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                    NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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PGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRFSNKAMS 367
                                                                                                                                                                                                     419 SDPLLPVIQKAVQSSAEGKAR----VQSLLAIKAIFGDDLPDNSLFTARVTETYLSLLAH 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasal H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizouchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishiuo Y., Oshima T., Saito N., Sampei G., Seki Y., Saivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horluchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-K12 / BHB2600;
Richterich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison K.,
                       MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Slalby M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                               DQTLR1ASDGCSKVQVFWTETVR--RAIEDKRDLSR1AFG1ASYLEMLRGRDEKGGTYES
                                                                                                                                                               SEP------TYGDAEWKLAKADDFESSLKLPAFDGWRDLDTSELDQKVIVLRKIIREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."; DNA Res. 3:379-392(1996).
-!- SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                         P33029; P94760;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
HPPOCT-2001 (Rel. 40, Last annotation update)
HPPOCTHELICAL OXIGOREDUCTASE YELO (EC 1.-.-).
                                                                                                                                                                                                                                                                                                                                                                                              AA.
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EMBL; AE000306; AAC75233.1; --
EMBL; D90849; BAA15981.1; --
ECOGENE; EG12036; yeiQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequenc
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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STRAIN=K12 / MG1655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
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Query Match
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                                                                                                                Gaps
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                                                                                                                                SLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQILE-HAPDWAIVGVGLTGSDR
                                                                                                                                           SKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADP-EAVLKHLVDPAIRIV
                                                                                                                                                                                                                 SMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVM
                                                                                                                                                                                                                                                       SCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAA
                                                                                                                                                                                                                                                                  SGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLC
                                                                                                                                                                                                                                                                                                            FPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRFSNKAM
                                                                                                                                                                                                                                                                                                                                                    SDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schneider K.-H., Giffhorn F.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-mannitol + NAD(+) = D-fructose + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                        Length 488;
                                      Hypothetical protein; Oxidoreductase; NAD; Complete proteome. NP_BIND 27 38 NAD (BY SIMILARITY).
                                                                                                             Indels
                                                           48 48 L -> R (IN REF. 3).
488 AA; 54031 MW; 85F1BFEC7E75ECD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schneider K.-H., Giffhorn F., Kaplan S.; "Cloning, nucleotide sequence and characterization dehydrogenase gene from Rhodobacter sphaeroides.";
                                                                                         DB 1;
                                                                                                             80; Mismatches 176;
                                                                                        29.4%; Score 739.5; DB 1 37.7%; Pred. No. 2.9e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 30, Last sequence update)
(Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mannitol 2-dehydrogenase (EC 1.1.1.67) (MDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 1-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lydrogenase gene from Rhodobacter sp.
Gen. Microbiol. 139:2475-2484(1993)
        Pfam; PF01232; Mannitol_dh; 1.
PRINTS; PR00084; MTLDHDRGNASE.
PROSITE; PS00974; MANNITOL_DHGENASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94075966; PubMed=8254318;
InterPro; IPR000669; Mannitol_dh
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1994
15-JUL-1998
                                                                                                            Matches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                      EP 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SI-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SI-4
                                                                                                                                                                                                                                                                                                                                                                                                                                         DP 424
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                                                 NP_BIND
CONFLICT
                                                                    SEQUENCE
                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 NVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQI--LEHAPDWAIVGVGLTGSDRSKK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAASGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 TEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRWDAGGKAFTVMSCDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 LVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRFSNKAMSDQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMDIQLVHAAMAHPLIAAFLHKVEVEEILPHVPPVPDTSIPDYLTLIESRFSNPEIADTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGI----ASYLEMLRGRDEKGGTYESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPTY ---- - GDAEW---- KLAKAD---- DFESSLKLPAFDGWRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAD (BY SIMILARITY).
A58247D6C7CCAF29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 725.5; DB 1;
Pred. No. 2.5e-42;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
12-JUN-2002 (Rel. 41, Last annotation update)
Darabinitol 4-dehydrogenase (EC 1.1.1.11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΑĄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80; Mismatches
                                                                                                                                                                                                                                                                                                       Pfam; PF01232; Mannicol_dh; 1.
PRINTS; PR00084; MTLDHDRGNASE.
PROSITE; PS00974; MANNITOL_DHGENASE; 1.
                                                                                                                                                                                                                                                                                    InterPro; IPR000669; Mannitol_dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                          18 29 N
476 AA; 51406 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.8%;
                                                                                                                                                                                                                                                          EMBL; AF018073; AAC45771.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 172; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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NP_BIND
SEQUENCE
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                                                                                                                                    STRAIN=CO-92 / Blovar Orientalis;

X MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.E., Titball R.W., Holden M.T.G.,
Parkhill J., Wren B.W., Thomson N.E., Thucher C., Mungall K.L.,
A Prentice M.B., Sebahim M., James K.D., Churcher C., Mungall K.L.,
A Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.W., Marlyshev A.W.,
A Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
A Feltwell T., Stevens K., Whitehead S., Barrall B.G.;
T. "Genome sequence of Yersinia pestis, the causative agent of plague.";
I "Genome sequence of Yersinia pestis, the causative agent of plague.";
I "Auture 413:523-527(2001).
C -I - CATATYTIC ACTIVITY: D-arabinitol + NAD(+) = D-xylulose + NADH.
C -I - SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APSGKSTVRVMGALRDYLLAPADPEAVLKHLV----DPAIRIVSMTITEGGYNINETTGA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 HQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 IEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRFSNKAMSDQTLRIASDGCSK 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 VHFGVGNFFRAHEAFYVEQILEHAPD-WAIVGVGLTGSDRSKKKAEEFKAQDCLYSLTET 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 FLGYAKARDPE-LAKWIEENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLVAEDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 IQWVIEDDFIAGRPALENVGAEMVTSVLPYEEAKIRILNASHSCIAWAGSLIGQCYIHES
                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.6%; Score 569; DB 1; Length 463; 36.0%; Pred. No. 1.2e-31; Live 71; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; NAD; Complete proteome.
SEQUENCE 463 AA; 51984 MW; D82E8988685B5EDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR000669; Mannitol_dh.
Pfam: PF01232; Mannitol_dh; 1.
PROSITE: PS00974; MANNITOL_DHGENASE; FALSE_NEG.
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15-JUN-2002 (Rel. 41, Created)
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                                                                                                                     SEQUENCE FROM N.A.
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TID DALD_K1
AC 052720;
DT 15-JUN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLTETAPSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYNINETTG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMSCDNLRHNG---NVAR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 PGIVHFGVGNFFRAHEAFYVEQILEHAPD---WAIVGVGLTGSDRSKKKAEEFKAQDCLY 82
                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: D-arabinitol + NAD(+) = D-xylulose + NADH.
-!- PATHWAY: D-arabinitol catabolism; first step.
-!- SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 PVLLHIGAGSFHRAHQAWYLHRVNAAVPPGERWTLT-VGNIRDDMHATLA-ALAAQQGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Fenard C., Cunnac S., Demange N., Sapiner P., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Meissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLVAED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.2%; Score 583; DB 1; Length 46
35.9%; Pred. No. 1.3e-32;
ive 63; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47095425D4836342 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00084; WTLDHDRGNASE.
PROSITE; PS00974; MANNITOL.DHGENASE; FALSE_NEG.
Oxidoreductase; NAD; Complete proteome.
SEQUENCE 465 AA; 50630 MW; 4705942504836342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-70N-2002 (Rel. 41, Created)
15-70N-2002 (Rel. 41, Last sequence update)
15-70N-2002 (Rel. 41, Last annotation update)
12-30N-2002 (Rel. 41, Last annotation update)
DALD OR YPO2325
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MEDLINE=21681879; PubMed=11823852;
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Matches 142; Conservative
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P58709;
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DALD_YERPE
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EMBL; U25347; AAA66392.1; -
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Best Local Similarity 41.5%
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562, 83334
                                                                                                        Erwinia herbicola.
                                                                                                                                                                                                                                  STRAIN=ATCC 21434;
                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                   NCBI_TaxID=549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UXAB_ECOLI
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NON_TER
SEQUENCE
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UXAB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
  δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 NFRDVRPNLEAVGVEMVESVIPYEEAKIRILNASHSCIAWAGTLIGQQYIHESTLTDVIY 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 AIADRYVTEDVIPCL-GDNGIDLPTYRDVVLKRFTNPYIQDTNQRVAADGFSKIPAMIAP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYNINETTGAFDLEN 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 PEGEREYEEITSIQKLLPWQAGLQPLINEGANPQTKVIAFTVTEGGYYLN-TRHRLETSN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 AAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMSCDNLRHNGNVARKAFLGYAKA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 PDLQADLQGECK--TIYGTLARILEKRMADNAGPLTLLNCDNVRHNGERFHDGMVEFLQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 RDPE-LAKWIEENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLVAEDFHQWVLED 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDAIEDSELL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRFSNKAMSDQTLRIASDGCSKVQVFWTE 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 VHFGVGNFFRAHEAFYVEQILEHAPDWAIVGVGLTGSDRSKKKAEEFKAQDCLYSLTETA 88
                                                                                                                                                                                                                                                                                                                   Microbiology 144:1631-1639(1998).
-- CATALYTIC ACTIVITY: D-arabinitol + NAD(+) - D-xylulose + NADH.
--- PATHWAY: D-arabinitol catabolism; first step.
---- SUBUNIT: Monomer.
                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                              STRAIN-1033-5P14 / KAY2026;
MEDLINE-98304087; PubMed-9639934;
Heuel H., Shakeri-Grandani A., Turgut S., Lengeler J.W.;
"Genes for D-arabinitol and ribitol catabolism from Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.2%; Score 534; DB 1; Length 45
31.1%; Pred. No. 2.8e-29;
tive 85; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455 AA; 51022 MW; 2D446E5232778DD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
PRTMYS; PR00084; MTLDHDRGNASE.
PROSITE; PS00974; MANNITOL_DHGENASE; FALSE_NEG.
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
D-arabinitol 4-dehydrogenase (EC 1.1.1.11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF045245; AAC26498.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 114; Conservative
                                                                                    Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; NAD.
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                                                                                                                                                                                             SEOUENCE EROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 TLQECYQ 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVRRAIE 394
                                                                                                                                                    NCBI_TaxID=573;
                                                                                                                                Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 RSKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPAD-PEAVLKHLVDPAIRI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 VSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 KSLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQI-LEHAPDWAIVGVGLTGSD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 KLLSANATVPQWDRHNLVPRIVHLGFGAFHRAHQAVYADVLAARHSSDWGYIEVNLIGGE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P24214; P78064;
01-MAR-1992 (Rel. 21, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Altronate oxidoreductase (EC 1.1.1.58) (Tagaturonate reductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                             Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.1%; Score 354; DB 1; Length 228; 41.5%; Pred. No. 2.1e-17; Live 28; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 AA; 24588 MW; ODC5756A85FDF410 CRC64;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical protein in tutB 3'region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
PROSITE; PS00974; MANNITOL_DHGENASE; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 483 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Oxidoreductase; NP_BIND 48 59 NAD (BY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 MSCDNLRHNGNVARKAFLGYAKARD 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||| || || || MSCDNIPENGRVIAGVVCAYARQCD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Tagaturonate dehydrogenase).
UXAB OR B1521 OR 22184 OR ECS2128.
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STRAIN-K12 / W3110;
Mizobuchi K.;
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DR DR DR KW COR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-0157:H7 / KIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemoirhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                           Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Rasai H., Rashimoto K., Kimura S., Kitakwa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cherichia coli.";

Gen. Microbiol. 112:697-705(1986).

- CATALYTIC ACTIVITY: D-altronate + NAD(+) = D-tagaturonate + NADH.

- PATHWAY: Glucuronate pathway.

- INDUCTION: BY GALACTURONATE, TAGATURONATE AND FRUCTURONATE. ITS

EXPRESSION IS SUBJECTED TO CATABOLITE REPRESSION BY GLUCOSE.

- SIMILARITY: SOME, TO THE MANNITOL DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blanco C., Mata-Gilsinger M.; "A DNA sequence containing the control sites for the uxaB gene of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed=1120655;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                               STRAIN=K12 / MG1655;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland v Riley M., Collado-vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
Submitted (SEP-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-45 FROM N.A., AND SEQUENCE OF 1-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000249; AAC74594.1; --
EMBL; D90795; BAA15204.1; --
EMBL; AE005352; AAG56245.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D13327; BAA02586.1; -.
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                               SEQUENCE FROM N.A
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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 INETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMSCDNLRHNGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARKAFLGYAK - - ARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVAEDFHQWVLE------DQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 MLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRFSN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 KAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRD----LSRIAFGIASYLEMLRGRDEK 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYIKHQLLSIALNGMTK---FRTRILPQLLAGQKANGTLPARLTFALAALIAFYRG-ERN 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KLAKADDFESSL-KLPAFDG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 GETY----PVQDDAHWLERYQQLWSQHRDRVIGTQELVAIVLAEKDHWEQDLTQVP---G 458
                                                                                                                                                                                                                                                                                               89; Mismatches 200; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                          28 IVHFGVGNFFRAHEAFYVEQILEHAP-DWAIVGVGLTGSDRSKKKAE-----EFKAQDCL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thesis (1994), Heinrich-Heine University / Duesseldorf, Germany.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
Interpreto: IPRO00669; Mannitol_dh.
Pfam: PF01232; Mannitol_dh; 1.
Oxidoreductase; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
                                                                                                                                                                                                                                             Length 483;
                                                                                                                                                                     332 332. P -> L (IN REF. 2).
483 AA; 54808 MW; AFA4677CF35BC2E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Polyol:NADP oxidoreductase (EC 1.1.1.-) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gluconobacter oxydans (Gluconobacter suboxydans).
                                                                                                                                                                                                                                                                       Pred. No. 3.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 AA
                                                                                                                                                                                                                                             11.3%; Score 285;
                                                                                                                 : ::|| | |||:: |: || 459 LVEOVANDLD------AILEKGMREAV 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455 WRDLDTSELDQKVIVLRKIIREKGVKAAI 483
               EMBL; M15737; AAA24757.1; -. PIR; A46549; A46549. EcoGene; EG11065; uxaB. InterPro; IPR000669; Mannitol_dh.
EMBL; AP002557; BAB35551.1; -.
                                                                                                                                                                                                                                                                     23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 GGTYESSEPTYGDAEW-----
                                                                                                                                                                                                                                                                     Best Local Similarity 23.69
Matches 120; Conservative
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P80354:
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P09424;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21359325; PubMed-11466286; MR B-1787; MEDLINE-21359325; PubMed-11466286; MR B-1787; Medling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing "Genome sequence and comparative analysis of the solvent-producing J. Bacteriol. 183:4823-4838(2001).
-:-CATALYTIC ACTIVITY: D-mannitol 1-phosphate + NAD(+) = D-fructose
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acetobutylicum encoding a phosphotransferase system and a putative PTS-modulated regulator.";
Microbiology 147:75-86(2001).
                                                                                                                                                                                                                                                                                                                                                                        Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                             1 MITRETLKSLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQIL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Behrens S., Mitchell W.J., Bahl H.; "Molecular analysis of the mannitol operon of Clostridium
                                                                                                                          1 MITRETLKSLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQIL 49
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00974; MANITOL_DHGENASE; 1.

PROSITE; PS00974; MANITOL_DHGENASE; 1.

Oxidoreductase; NAD; Complete protecome.

NP_BIND 3 14 NAD (BY SIMILARITY).

SEOUENCE 384 AA; 43921 MW; 0F73B98AFD9B8F6C CRC64;
                  8EE7F5B6413497FD CRC64;
                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17).
                                                     Score 258; DB 1; 1
Pred. No. 9.2e-12;
                                        10.3%; Scc...
100.0%; Pred. No....
... 0; Mismatches
                                                                                                                                                                                                                                                   384 AA
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STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21097245; Pubmed-11160802;
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(Rel. 39, Last sequ
(Rel. 40, Last anno
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PRINTS; PR00084; MTLDHDRGNASE
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                  5648 MW;
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Matches 101; Conservative
                                                                                         Conservative
                                                                                                                                                                                                                                                     STANDARD;
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                                                                      Best Local Similarity
Matches 49; Conserv
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50 AA;
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SEQUENCE
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Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.; "Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes."; Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                            307 FPGILVGYENVDDAIEDSELLGNLKNYLNKDVI----PTLKAPSG-----MTLEGYRDS 356
                                                                                                                                                                                                                                                                                                                                                                                                      224 YLGYLKGYKYIHEAIKDKE-----INKIIVGFHSEAVQALSEKHKIDIQILKEYSNK 275
                                                                                                                                                                                                                                  256 VAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYV-----KIRMLNAGHVMLC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 VISRFSNKAMSDQTLRIASDGCSKVQV--FWTETVRRAIEDKRDLSRIAFGIASYLEMLR 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 LLKRFENEYLKDDVSRVGRDPMRKLSSNDRLITPLKLCCDLKIDFTNILFGVAS----- 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----- DEKAQGIQNII 348
                                           76 KAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGY 135
                                                                                                                        136 NINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMSCDNLRHNG 195
                                                                                                                                                                 -----ELLRGF----LKKRSEINDKPLDIIACENALFAS 127
4 LHFGAGNIGRGFIGYLLYKSNYETTFVDIFDKVVDDINKYKRYTVITLSTSKNKEKVENV 63
                                                                                    ------KDSVALEKEVLE-----ADLITTSLGL
                                                                                                                                                                                                            196 NVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPL
                                                                                                                                                                                                                                                                                                                    Davis T., Yamada M., Elgort M., Saier M.H. Jr.; Nucleotide sequence of the mannitol (mtl) operon in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-1989 (Rel. 10, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17).
MTLD OR B3600
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SEQUENCE FROM N.A., AND REVISIONS.
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STRAIN-K12 / MG1655;
MEDLINE-94316500; Pubmed-8041620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88288055; PubMed=3135464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 ----GYLFNYKE-
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91 NNLKSTG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 TLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYESSEPT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 AFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMSCDNLRHNGNVARKAF 202
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                                                                                                                                                                                              and D-glucitol-6-phosphate dehydrogenase from Escherichia coli.";
J. Bacteriol. 159:986-990(1984).
-!- CATALYTIC ACTIVITY: D-mannitol 1-phosphate + NAD(+) = D-fructose
                                                                                                                                                          Novotny M.J., Reizer J., Esch F., Saier M.H. Jr.; "Purification and properties of D-mannitol-1-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 VHFGVGNFFRAHEAFYVEQILEHAPDWAIVGVGLTGSDRSKKKAEEFKAQDC--LYSLTE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QWVLE-DQFADGRPPLEKAGV@MVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDA
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Oxidoreductase; NAD; Complete proteome.
NP_BIND 3 14 NAD (BY SIMILARITY).
CONFLICT 86 86 A -> R (IN REF. 1 AND 2).
SEQUENCE 382 AA; 41139 MW; 1AC44028C150A7B2 CRC64;
                                                    Figge R.M., Ramseier T.M., Saier M.H. Jr.;
"The mannitol repressor (MtlR) of Escherichia coli.";
J. Bacteriol. 176:840-847(1994).
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6.5e-07;
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21.9%; Pred. No. 6
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EMBL; X06794; CAA29954.1; ALT_SEQ.
EMBL; U03845; AAA92661.1; -.
                                                                                                                        SEQUENCE OF 1-25.
MEDLINE=85006766; PubMed=6384188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EcoGene; EG10616; mtlD.
InterPro; PPR00669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; l.
PRINTS; PR00084; MTLDHDRGNASE.
                                   MEDLINE=94131964; PubMed=8300537;
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PIR; S10394; S10394
PIR; S12240; S12240
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--RQPLRKLSAGDRLIKPLL-----GTLEYGLPH 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| : | ||: : | ||: : ||: || ||: : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning, expression, and isolation of the mannitol transport protein from the thermophilic bacterium Bacillus stearothermophilus.";
J. Bacteriol, 178:5586-591(1996)
J. CATALYTIC ACTIVITY: D-mannitol 1-phosphate + NAD(+) = D-fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 YITKAHLITTAVGPHILPAIATILAEGLOKRITINKTPLHIIACENMIGGSDVLKSHVFE 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 AAVKADL----KNPEKPSTVFGYVVEALRRRWDAGGKAFTVMSCDNLRHNGNVARK-AFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLEDQFADGR-PPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCFPGILVGYENVDDAIE
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                                                                                               430 YGDAEWKLAKADDFESSLKLPAFDGWRDLDTSELDQKVIVLRKIIREKGVKAAI 483
                                                                                                                                                                   -----SEDDPQAQELAALIADKGPQAAL 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6-phosphate + NADH.
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6A60B887A8C20052 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17).
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21.0%; Pred. No. 1.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Geobacillus.
                                                                                                                                                                                                                                                                                                                                          382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
PRINTYS; PR00084; MILDHDRGNASE.
PROSITE; PS00974; MANNITOL_DHGENASE; 1.
                                                                                                                                                                                                                                                                                                                                             PRT;
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382 AA; 43167 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 35, Created)
(Rel. 35, Last seq
                                                                                                                                                                   322 KNLIE-GIAAAMHFR-----
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nes 99; Conserv
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                            290 VERVG---
                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997
01-NOV-1997
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AIAEADL.VTTAIGPNILPRIAELIAQGIDARAEANCQNGPLDIIACENM-----IGGSTF 132

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences of the enzyme IIIMII gene and the mannitol-1 phosphate dehydrogenase gene, expression in Escherichia coli, and comparison of the gene products with similar enzymes.";
J. Bacteriol. 173:3709-3715[1991].
                                                     ----RSPIRKLGANDRLIGPATOYYDLFG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 PSGKSTVRVMGALRDYLLAPADPEAVLKHLVDPAIRIVSMTITEGGYNINETTGAFDLEN 148
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    ---EGYRDSVISRFSNKAMSDQTL 371
                                                                                                                                                               RIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYESSEPTYG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | : | : | : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65; Mismatches 144; Indels 112;
                                                                                                                                                                                                                                                                                                                                       DAEWKLAKADDFESSLKLPAFDGWRDLDTSELDQKVIVLRKIIREKGVKAAI 483
                                                                                                                                                                                                                                                                                                                                                                                   319 QVPHGLVK-----GIAALLEP-----YENDEEAVALQKTIQETGVEGAL 358
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357 AA; 39864 MW; C457FC37EF2D4C27 CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Mannitol-1 phosphate 5-dehydrogenase (EC 1.1.1.7).
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InterPro; IPR000669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
PRIWTS; PR00084; WTLDHDRONASE.
PROSITE; PS00974; MANNITOL_DHGENASE; 1.
DSELLGNLKNYLNKDVIPTLKAPSGMTL----
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MEDLINE=91267934; Pubmed=1904856;
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Best Local Similarity 21.7
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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MTLD_ENTFA
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LAEEVAIIFEKPSLSEQWI----GFPDAAVDRIVPLOKHK-------DPLFVQVE 176
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                                                                                                                                                          -- EGYRDSVISRFSN 363
                                                                             DFHQWVLEDQFADGRPPLEKAGVQMVGDVT----DWEYVKIRMLNAGHVMLCFPGILVGY
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282 KYISDAITRVARTPIRKL-----GAQERFIRPIRELQERNLVSAAFIAMI 326
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Perfect score:

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09wxs3 thermotogia
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09xi5 yersinia pe
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Q8zm58 salmonella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLTGSDRSKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADPEAVLKHLVD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning of a gene for D-Sorbitol dehydrogenase from Gluconobacter oxydans G624 and expression of the gene in Pseudomonas putida IFO3738.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gluconobacter oxydans (Gluconobacter suboxydans).
Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae; Gluconobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2516; DB 2; Length 485; Pred. No. 1.5e-173; 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biosci. Bioeng. 89:463-468(2000).

EMBL; AB028937; BAA99414.1; -
InterPro; IPR000669; Mannitol_dh.

Pfam: PF01232; Mannitol_dh; 1.

Pfam: PR00084; MTLDHDRGNASE.

SEQUENCE 485 AA; 53642 MW; A7C363D728EEA7DC CRC64;
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Last annotation update)
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                                                   Q8UA45
Q8ZM58
Q98JL8
Q9XBD5
                                                                                                                              Q8R8Q5
Q93RC4
Q9WXS3
Q9CE49
Q97L67
Q97L67
Q9KF17
Q8K1CS0
Q8RCS0
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Q9KH90
Q8XDG9
Q9K2Y2
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098355 pseudomonas
098355 pseudomonas
098269 rhizobium 1
08x516 escherichia
08x506 escherichia
068111 rhodobacter
092007 rhizobium m
082626 salmonella
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Q8zgk9 yersinia pe
Q8xe83 secherichia
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Q8vuu5 gluconobact
                                                                                                                      8, 2003, 16:28:22 ; Search time 38 Seconds (without alignments) 2629.812 Million cell updates/sec
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2516
1 MITRETLKSLPANVQAPPYD.......KVIVLRKIIREKGVRAAIPA 485
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             GenCore version 5.1.4\_p5\_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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score greater than or equal to
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Maximum DB seq length: 200000000
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sp_rodent:*
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PAIRIVSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGG
                                          KKLNAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNA
                                                                              GHVMLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISR
                                                                                                              PAIRIVSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGG
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         KAFTVMSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIA
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                                                                                                                                                                                                                                                                                                                               Gluconobacter oxydans (Gluconobacter suboxydans).
Bacteria: Proteobacteria: alpha subdivision; Acetobacteraceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53541 MW; 883EC4956B3C6CF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Shinjoh M., Tazoe M., Hoshino T.;
"NabPH-Dependent L-Sorbose Reductase Is Responsible in Sasimilation in Gluconobacter suboxydans IFO 3291.";
J. Bacteriol. 184:861-863(2002).
EMBL. AB063188; BAB83933.1;
InterPro: IRR000669; Mannitol_dh.
PRINTS; PR00084; MTLDHDRGNASE.
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Last annotation update)
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MEDLINE=21650687; PubMed=11790761;
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                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                  GHVMLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISR
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Local Similarity 45.2%; Pred. No. 2.6e-58;
es 199; Conservative 66; Mismatches 171;
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PROSTIE; PS00974; MANNITOL_DHGENASE; 1.
COMDLETE PROLEOME.
SEQUENCE 491 AA; 54350 WW; 8729A9F7.
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InterPro, IPR000669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
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Nature 406:959-964(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: A MANNITOL DEHYDROGENASE WITH A BROAD SUBSTRATE SPECIFICITY: SUBSTRATES INCLUDE MANNITOL, ARBHITOL AND SCREITOL, THESE ARE OXIDIZED TO GIVE THE CORRESPONDING KETO SUGARS. THIS ENZYME WILL ALSO CATALYZE THE REDUCTION OF FRUCTOSE AND XYLULOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bruenker P., Altenbuchner J., Mattes R.; Structure and function of the genes involved in mannitol, arabitol and glucitol utilization from Pseudomonas fluorescens DSM50106."; Gene 206:117-126(1998)
GKAFTVMSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEI
             -!- MISCELLANEOUS: THE MTLD PROTEIN IS ENCODED BY THE MTL EFGKDYZ OPERON THIS OPERON ENCODES PROTEINS FOR THE UPTAKE AND UTILIZATION OF MANNITOL, ARABITOL AND SORBITOL.
-!- SIMILARITY: BELONGS TO THE MANNITOL DEHYDROGENASES FAMILY.
EMBL: AF007800, AAC04472.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: D-MANNITOL + NAD(+) = D-FRUCTOSE + NADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- INDUCTION: BY MANNITOL, ARABITOL AND SORBITOL. NOT INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bruenker P., Altenbuchner J., Kulbe K.D., Mattes R.; "Cloning, nucleotide sequence and expression of a mannitol dehydrogenase gene from Pseudomonas fluorescens DSM 50106 in Escherichta coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., CHARACTERIZATION, AND SEQUENCE OF 1-20
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7C12DFA443CEA443 CRC64;
                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Mannitol 2-dehydrogenase (EC 1.1.1.67) (MDH).
                                                                                                                                                                                                                                                                                                  493 AA
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Pfam; PF01232; Mannitol_dh; 1.
PRINTS; PR00084; WILDHDRGNASE.
PROSITE; PS00974; MANNITOL_DHGENASE; 1.
Oxidoreductase; NAD.
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MEDLINE-98121321; PubMed-9461423;
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                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas fluorescens
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NCBI_TaxID=294;
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                                                                                                                                                                               VGLTGSDRSKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADPEAVLKHLV 119
                                                                                                                                                                                                         DPAIRIVSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAG 179
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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  Length 493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.7%; Score 797; DB 16; 39.3%; Pred. No. 2.8e-49; iive 72; Mismatches 187;
35.3%; Score 888; DB 2; 42.2%; Pred. No. 7.4e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
                       Pred. No. 7.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492
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PROSITE; PS00974; MANNITOL_DHGENASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21082930; PubMed=11214968;
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EMBL; AP003005; BAB51465.1; -
InterPro; IPR000669; Mannitol_dh
Pfam; PF01232; Mannitol_dh; 1.
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Matches 174; Conservative
                                             Conservative
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                       Similarity
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GVSYTIPDP 429
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SEQUENCE 492 AA
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                       Best Local Sim
Matches 181;
  Query Match
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LTGSDRSKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADPEAVLKHLVDP 121
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Q8X516;
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                                                                                                                                                                              119 VDPAIRIVSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDA 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 KRFSNPKIGDTIRRLCLDGSNRQPKFIIPTIADRLKAGKGVAGLALESALWCRYCFGTSD 419
                                                                                                                                          VGL-TGSDRSKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADPEAVLKHL 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cowie A., Gouzy J.,
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Golding B., Puehler A.;

"The complete sequence of the 1,683-kb pSymB megaplasmid from the h fixing endosymbiont Sinorhizobium meliloti.";

Froc. Natl. Acad Sci. U.S.A. 98:9889-9894(2001).

EMBL; AL603647; CAC49841.1;

InterPro; IPR000669; Mannitol_dh.

PROSTIE: PS00974; Mannitol_DhG.

Oxidoreductase; Plasmid; Hypothetical protein; Complete protecome.
                                                         GGKAFTVMSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAE
                                                                                                                                                                                                                                                                                                                                                                                                         180 GIVPFIVMSCDNIPHNGHVISDGVIGLARLIDEDLAGWVSSNVAFPNGMVDRITPATTDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 ERGILAKDEGVEDAWPVECEPFRQWVLEDHFTDGRPPLEKVGVQFVRDVAPYELMKIRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAGHVMLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVI
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                           ITRETLKSLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQILEH--APDWAIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 IAKKLNAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         imid; Hypothetical protein; Complete proteome
52925 MW; 39739B73874ED79B CRC64;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative D-mannonate oxidoreductase protein (EC 1.1.1.57).
UXUB OR RB1441 OR SMB20749.
Rhizobium meliloti (Sinorhizobium meliloti).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  487 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Best Local S
Matches 166
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STRAIN-015:H7 / RIMD 0509952;
MEDLINE-21156231; PubWed-11258796;
MEDLINE-21156231; PubWed-11258796;
MEDLINE-21156231; PubWed-11258796;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
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                                                                                                                          182 AFTVMSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAK 241
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BELINE-21074935; Pubmed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Grosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Amelor R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";

Nature 409:529-533(2001).
                                                                                                                                                                                                                                  242 KLNAASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAG
                                                                                                                                                                                                                                                                                          HVMLCFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRF
L----RSPETRDALHPQDGLYTLAVQDGEG-SELSVVGSVVELLCAPDDPEAVLRRMADP
                                        122 AIRIVSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGK
                                                                                                                                                                                                                                                                                                                                 297 HSTLAYLGYLAGAETVADAMALAGMEALVEGLMRHEVSPTLPELPGFDLPAYRAELLQRF
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Mannonate oxidoreductase (D-mannonate oxidoreductase)
UVUB OR Z5921 OR ECS5282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          486 AA
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PRINTS; PR00084; MTLDHDRCNASE.
PROSITE; PS00974; MANNITOL_DHGENASE; 1.
Complete proteome.
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EMBL; AP002569; BAB38705.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli O157:H7.
Bacteria; Proteobacteria;
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Ogasawara N., Yasunaga T.,

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GAKATV 480
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                                                                                                                                                                                 Matches 184;
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                                                                                                                                                                                           MSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNA 245
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                                                                                                 RSKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADP-EAVLKHLVDPAIRI 125
                                                                                                                                              126 VSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTV 185
                                                                                                                                                                                                                                        246 ASGLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVML 305
                                                                                                                                                                                                                                                                                     CFPGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRFSNKA 365
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                                Gaps
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MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
                                                    SLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQILEHA-PDWAIVGVGL-TGSD
                                                                 MSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYES
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STRAIN-0157:17 / EDD5933 / ATCC 700927;
MEDLINE-21074935; Pubmed-11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                               17;
        Length 486;
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Last annotation update)
        16;
      30.8%; Score 775.5; DB 1
36.4%; Pred. No. 9.9e-48;
iive 87; Mismatches 205
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01-JUN-2002 (TEMBLEEL. 21
01-JUN-2002 (TEMBLEEL. 21
PUTATIVE OXIGOZEGE.
YDEI OR 22155 OR EGS2151
Escherichia coli 0157:H7.
                              Conservative
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Matches 177;
        Query Match
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Q8X506;
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DQTLRIASDGCSKVQVFWTETVR--RAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTYES 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMS 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |-| SDPLLPVIQKAVQSSAEGKAR----VQSLLAIKAIFGGDLPDNSLFTAKVTEAYLSLLAH 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vicek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.; "Sequence of a 189-kb segment of the chromosome of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 LPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQI-LEHAPDWAIVGVGLTGSDRS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCF
RA Kuhara S., Shiba T., Honda T., Sasakawa C., Ogasawara N., Yasuni RT Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RT "Complete genome sequence of enterohemorrhagic Escherichia coli RT Ol75:H7 and genomic comparison with a laboratory strain K-12.";

RL DNA Res. 8:11-22(2001).

DR EMBL; ABC002557; BAB35574.1; -

DR EMBL; ABC002557; BAB35574.1; -

DR EMBL; APC00257; BAB35574.1; -

DR FINEL; RPC00257; BAB35574.1; -

R FINTS; PR00084; MILDHDRGNASE.

R PROSITE; PS00974; MANNITOL_DHGENASE; 1.

R Complete proteome.

D SEQUENCE 486 AA; 53581 MAN.
                                                                                             comparison with a laboratory strain K-12.";
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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Mannitol 2-dehydrogenase (EC 1.1.1.67).
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Salmonella.
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Q82626;
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                                                                                                                                                                                                                                            CDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAAS 247
                                                                                                                                                                                                                                                                                                                                           GLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCF 307
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                                                                                                                                                                                                                                                                              128 MIITEGGYNINETTGAFDLENAAVKADLKNPEKPSTŲFGYVVEALRRRWDAGGKAFTVMS 187
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                                                                                                                                                                                            Gaps
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Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                PGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRFSNKAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Last Sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable mannitol 2-dehydrogenase protein (EC 1.1.1.67).
MTLK R02440 OR SMC015610.
Rhizobium mellloti (Sinorhizobium mellloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                    22;
                                                                                                                            Length 478;
                                                                                                                                                    84; Mismatches 202; Indels
                                                                                                    478 AA; 51442 MW; 8427F89B6F2A4F38 CRC64;
             U.S.A. 94:9384-9388(1997).
                                                                                                                            Score 768; DB 2;
Pred. No. 3.3e-47;
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                                                                                                                          30.5%; Score 768; 36.4%; Pred. No. 3
                                                             PRINTS; PR00084; MTLDHDRGNASE.
PROSITE; PS00974; MANNITOL_DHGENASE; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
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                                    InterPro; IPR000669; Mannitol_dh.
capsulatus SB1003.";
Proc. Natl. Acad. Sci. U.S.;
EMBL; AF010496; AAC16201.1;
                                                  Pfam; PF01232; Mannitol_dh;
                                                                                                                                         Best Local Similarity 36.4
Matches 176; Conservative
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                                                                                                     SEQUENCE
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Q92N07
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Daviss P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Haque A., Hien T.T., Holroyd S., Jagels K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --KEIVFNDANADRLHAAAVAAKDDPMAFLALS--DIFGDVAQSDLFRRFAHALKVLWE 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 AIAYPAALLDIHFVHEAMEEPLIRAFLSKLEHDEIIPVIPPVPDTDLKDYYKLIETRFSN 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 KAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKGGTY 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 PKIGDTVARLAQDGSNRQPKFILPSTADRLRRGEDVVGLSLVSALWCRYFAGKSDSG--- 421
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 TLKSLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQI--LEHAPDWAIVGVGLT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIVSMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAF
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                            Length 494;
"Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591790. CAC47019.1;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                    Oxidoreductase; Complete proteome.
SEQUENCE: 494 AA; 53822 MW; 7533287D8EF58F24 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
putative D-mannonate oxidoreductase (EC 1.1.1.57).
                                                                                                                                                                                                                                                                                                                                                                       83; Mismatches 208;
                                                                                                                   Interpro; IPR000669; Mannitol_dh.
Pf01232; Mannitol_dh; 1.
PROSITE; PS00974; MANNITOL_DHGENASE; ÜNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.3e-46;
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MEDLINE=21534947; Pubmed=11677608;
                                                                                                                                                                                                                                                                                                            30.2%;
                                                                                                                                                                                                                                                                                                                                                                 Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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SEQUENCE FROM N.A.
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KGTRATL 484
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Courtney L., Porwollik S., Ali J., Dante M., Du F.
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MEDLINE-21534948; PubMed-11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
                                                                                                                                                                                                                                                       KKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADP-EAVLKHLVDPAIRIVS 127
                                                                                                                                                                                                                                                                                                     MITTEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVMS 187
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                                                                                                                                                                                                                        10 LPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQI-LEHAPDWAIVGVGLTGSDRS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                          PGILVGYENVDDAIEDSELLGNLKNYLNKDVIPTLKAPSGMTLEGYRDSVISRFSNKAMS
                                 "Complete genome sequence of a multiple drug resistant Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative mannitol dehydrogenase.
YDFI OR STM1508.
Salmonella typhimurium.
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
  S., O'Gaora P., Parry
                                                                                                                                                               DB 16; Length 488;
            Simmonds M., Skelton J., Stevens K.
                                                                                                                                                                                     Indels
                                                                                                   PRINTS; PRO0084; MTLDHDEGNASE.
PROSITE; PS00974; MANNITOL_DHGENASE; 1.
Oxidoreductase; Hypothetical protein; Complete proteome.
SEQUENCE 488 AA; 53922 MW; 18F64DE2ACCA7781 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                              30.2%; Score 759.5; DB 16;
llarity 36.3%; Pred. No. 1.4e-46;
Conservative 87; Mismatches 205;
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Krogh A., Larsen T.S., Leather S., Moule
Quail M., Rutherford K., Simmonds M., Ske
Whitehead S., Barrell B.G.;
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                                           enterica serovar Typhi CT18.";
Nature 413:848-652(2001).
EMBL; ALG57270; CAD01805.1; -1
InterPro; IPR000669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                       Best_Local Similarity
Matches 175; Conserv
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SV 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLDDDLPLVAEDFHQWVLEDQFADGRPPLEKAGVQMVGDVTDWEYVKIRMLNAGHVMLCF 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LSAKATLPDYDRAALAARMVHLGFGAFHRAHQGVYTDILAAEQHSDWGYYEVNLIGGE-- 63
                                                                                     "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQI-LEHAPDWAIVGVGLTGSDRS 68
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Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
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                                                                                                                                                                                                                                                                                                                                              DB 16; Length 488;
                                                                                                                                               EMBL; AE008765; AAL20427.1; -
InterPro; IPR000669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
PR1175; PR00084; WTLDHDRGNASE; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 488 AA; 53896 MW; 704BF8C27F4407A6 CRC64;
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U-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative D-mannonate oxidoreductase.
                                                                                                                                                                                                                                                                                                                                       30.0%; Score 755.5; DB 1
36.3%; Pred. No. 2.8e-46;
iive 86; Mismatches 206
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MEDLINE=21470413; PubMed=11586360;
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 36.3
Matches 175; Conservative
                                                                                                                                Nature 413:852-856(2001)
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SEQUENCE FROM N.A.
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Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Leathwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Oyston P.C.F., Quall M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague.";
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                                                                                                                                                                                                                                                                                                                                                                        SMTITEGGYNINETTGAFDLENAAVKADLKNPEKPSTVFGYVVEALRRRWDAGGKAFTVM 186
                                                                                                                                                                                                                                                                                                                                                                                               SLTITEKGYCIEPGTGQLDLQNEFIRADLAVPNAPTSAPGVLVEALRLRRLRGLPPFTVL 183
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                   SLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQILE-HAPDWAIVGVGLTGSDR
                                                                                                                                                                                                                                                                                    SCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSAEIAKKLNAA
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01-JUN-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative oxidoreductase.
Fig. 08 23431 OR E233064.
Escherichia coli 0157:H7.
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae:
NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
                                                                                                                                                                                                                    Length
                                                                                                                                                   PRINTS; PR00084; WTLDHDRGNASE.
PROSTTE; PS00974; MANUTOL_DHGENASE; 1.
HYPOTHELICAL PROTEIN; COMPLETE PROTECOME
SEQUENCE 490 AA; 54006 MW; FC35D50FF011DC73 CRC64;
                                                                                                                                                                                                                    DB 16;
                                                                                                                                                                                                                                            190;
                                                                                                                                                                                                                    29.9%; Score 753.5; DB 1
37.8%; Pred. No. 3.9e-46;
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                                                                                                                                                                                                                 Query Match
Best Local Similarity 37.8<sup>th</sup>
Matches 171; Conservative
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                                                                                                    Nature 413:523-527(2001)
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
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                                                                             Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
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Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L. Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
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Putative D-mannonate oxidoreductase (EC 1.1.1.57).
Salmonella typhimurium, and
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PRIMIS; PR00084; MTCHDRCNASE.
PROSTIE: PS00094; MANNITOL_DHGENASE; 1.
Complete protecome.
                                                                                                                                                                                                                                    STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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Matches 159; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Bashaman D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 TGSDRSKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADPEA-VLKHLVDP 121
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Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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PROSITE; PS00215; MITOCH_CARRIER; UNKNOWL.1.
OXIGOREGUCIASE; Hypothetical protein; Complete proteome.
SEQUENCE 490 AA; 54007 WW, A521610BB383A9FF CRC64;
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Interpro: IPR000669; Mannitol_dh.
Interpro: IPR001993; Mitoch_carrier.
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SPECIES-S.typhi; STRAIN-CT18;
MEDLINE-21534947; Pubmed-11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:848-852(2001).
EMBL; AE008844; AAL22010.1; -.
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                                                                                 NCBI_TaxID=602, 601;
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Best Local Similarity
Matches 156; Conserv
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Search completed: May 8, 2003, 16:33:38
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Title: Perfect score: Sequence:	US-09-926-163B-1 4115 1 aagcttgcatgcctgcaggttccggggcgggcctgaagctt 4115
Scoring table:	OLIGO_NUC Gapop 60.0 , Gapext 60.0 ·
Searched:	2054640 seqs, 14551402878 residues
Word size :	0
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES Description		8937		AX25642	AJ238981	I09132 Se	AJ000333 Mycobac		AF027128	AF102233 Transposo	AF076213 Promoter		002455 CLOning vec	A2591/ Expression A25918 Expression	G49583 SHGC-60412	AR007549 Sequence	AR029479 Sequence	190222 Sequence 10 G63570 SHGC-141568	U13871 pT7T3D clon	E49323 Infectious	002437 Cloning vec	AROZ/100 Sequence ARO36062 Sequence	AR160052 Sequence	AR209764 Sequence	AF129072 Cloning v	AF069723 Expressio	AF069724 Expressio	U02433 Cloning vec	AF069722 Expressio	U02442 Cloning vec	AX195206 Sequence	· ·	DOZ430 CICHING VEC	6 6	3383 Sequenc	2583	AR198722 Sequence AR169417 Sequence	amanhac (Troo	SNTS		DNA linear BCT	sorbitol denydrogenase, complete		ain:G624) DNA.		subdivision; Acetobacteraceae;	ıra,M., Takata,Y., Noguchi,Y.,	
SUMMARIES		AB028937	SYNITEOR	AX256425	DRE238981	109132	MTGLMS .	SYNCATBLI	AF027128	AF102233	AF076213	XXU02428	002455	A2591/ A25918	G49583	AR007549	AR029479	190252	XXU13871	E49323	XXU02437	AR036062	AR160052	AR209764	AF2/6982 AF129072	AF069723	AF069724	XXU02433	AF069722	U02442	AX195206	002451	AF069717	- 1 ∴	933	25	AR198722 AR069417	,	ALIGNMENTS		407	s gene ror	48	e. (str		eria; alpha	,C., Matsuura,M	
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                                                                                                                              ACTGGGCGATTGTTGGTGTTGGCCTGACGGCCAGTGACCGTTCAAAGAAAAAAGCCGAGG
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                                                                                                                                                                                                                                                                                                                                              ENATFPNGMVDRITPTVSAEIAKKLNAASGLDDDLPLVAEDFHQWVLEDGFADGRPPL
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IEDKRDLSRIAFGIASYLEMLRGRDERGGTYESSEPTYGDAEWKLAKADDFESSLKLP
AFDGWRDLDTSELDOYVLKRIIRREGVKAAIPA"
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 D-Sorbitol dehydrogenase from Gluconobacter
                                          2 (bases 1 to 4073)
Shibata,T. and Saito,Y.
Direct Submission
Submitted (15-JUN-1999) Takashi Shibata, Fujisawa Pharmaceutical
Co., Ltd., Fermentation Development Laboratories, Shinkawa-cho,
Nakagawara 156, Nishikasugai-gun, Aichi 452-0915, Japan
(E-mall:takashi_shibata@po.fujisawa.co.jp, Tel:81-52-401-0275,
Fax:81-52-400-1380)
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/codon_start=1
/transl_table=11
/product="sorbitol dehydrogenase"
/protein_id="BaA99414.1"
/db_xref="GI:9049449"
of a gene for D-Sorbitol dehydrogen G624 and expression of the gene in
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Pred. No. 0;
0; Mismatches 0;
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                                      463-468
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501. .1958
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CTAGCGATGGCTGTTCCAAGGTTCAGGTGTTCTGGACGGAAACCGTGCGTCGGGC 	1837 AATGGAAGTTGGCCAAGGCGGACGACTTCGAAGCTCTCTGAAGCTCCCGGCGTTCGATG 1896 1801 AATGGAAGTTGGCAAGGCGGACGACTTCGAAGCTCTCTGAAGCTCCCGGCGTTCGATG 1860 1801 GATGGAAGTTGGCAAGGCGGACTGCATCAAAGCTCTCTGAGCTGCCGGCGTTCGATG 1860 1897 GGTGGCGCGATCTGCATAGCGCCGAACTGCATCAAAAGGTCATCGTGCTGCGGAAGATCA 1956 1861 GGTGGCGCGATCTGGATACGTCCCGAACTGGATCAAAAGGTCATCGTGCTGCGGAAGATCA 1920 1861 GGTGGCGCAACTGGATACGTCCCGAACTGGATCAAAAGGTCATCGTGCTGCGGAAGATCA 1920		CCATT 210 AGTCC 219 AGTCC 216 STTTC 225	CGTAGGGCGCGAAAGATCAAAGCTGGTCTGTGTTCCGGGTGTCTAAAAAGTTTC ZZ CGTAGGGCGCGAAAGATCAAAGCTGTCGGTCGCTTAATCCGGTCCCAAGCCGCTTG Z3 [AGCACGTCCGGATGATGTCGGGATCAGGGTCTGTCTCTGTGATGGTTTCTGGGCC 254 AGCACGTCCGGATGATGTTCGCGGATCAGGGTGCGCCAGCGCAGGGGATTTCTGTGTCA 243 AGCACGTCCGGATGATGTTGCGGGATCAGGGTGCGCCAGCGCAGCGCGGGATTTCTGTGTCA 240 GTTGCGCTGCGGGTGATGCCGAGAATACGATACGGATCCGGCTGCGGGGGGG 249 GTTGCGCTGCGGGTGATGCCGAGAATACGATACGCATCCGGCTGCTGTTTCTGCTGCCCGGGGGGGG	CGATTGTTGCCGCTTTCGCCCGGTCCCATGCTCCGCCCCCTCGTTTCCGCTGGCGCGCCCCCTGTTTGTTG	231 ACCCCATACGCAACACTITCCTTCGGGGGGCGCGGGCTGGGGCCGGCATTCGCGCATTCGCGGCTGGGGCGCGGGGGCGGGGGGGG

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IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVE
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synthetic construct
artificial sequences.

1 (bases 1 to 91)
Hasan,N., Kur,J. and Szybalski,W.
An MboII/FokI trimming plasmid allowing consecutive cycles of precise 1 to 12-base-pair deletions in cloned DNA
Gene 82 (2), 305-311 (1989)
                                                                                                                                                                                                                                                                                                                                    Length 4643;
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4269- 4640
/note="polyadenylation signals"
1047 q 1225 t
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Mismatches
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                                                                                                 /product="beta-lactamase"
/protein_id="AABB3990.1"
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Sequence 9 from Patent WO0076523.
AX256425
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                  complement(3277. .4137)
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/organism="synthetic cc
/db_xref="taxon:32630"
26 c 25 g
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complement(3277.
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1 (bases 1 to 360)
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                                                                  /gene="bla'
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Best Local Similarity 100.
Matches 40; Conservative
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AHIEVDITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLOFFMPVLGALFIGVAV
APANDIYNERELLNSMGISQPTVVFVSKKGLQKILNVQKKLPIIQKIIIMDSKTDYQG
                                                                                                                                                   3960
FQSMYTFVTSHLPPGFNEYDFVPESFDRDKTJALJMNSSGSTGLPKGVALPHRTACVR
FSHARDPJFGNQJJPDTAJLSVVPFHHGFGMFTTLGYLJCGFRVVLMYRFEEELFLRS
                                                                                                                                                                                                                                                                                                                                                                 circular SYN 08-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression vector pTATALUC+.

Expression vector pTATALUC+

Expression vector pTATALUC+

Expression vector pTATALUC+

(bases 1 to 4643)

Altschmied, J. and Duschl, J.

Set of optimized luciferase reporter gene plasmids compatible with
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AKKLRGGVVFVDEVPKGLTGKLDARKIREILIKAKKGGKIAV"
                                                                                  3841 AAGCCCATTGTGCGGTTTCGGAAACATCAGGGTCCGGATCACTCAGCAGCTCCCGCGCAG
                                                                                                                                    AAGCCCATTGTGCGGTTTCGGAAACATCAGGGTCCGGATCACTCAGCAGCTCCCGCGCAG
                                                                                                                 CGGTTGCGTCCAATCCGTTTGACCGGAGAGCCAGAAAAAAACGTCCGGAATGTCGCATTA
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Submitted (26-SEP-1997) Physiological Chemistry I/Biocenter,
University of Muerzburg, Am Hubland, Wuerzburg 97074, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                      AF027127 4643 bp DNA: circular SYN 08-1
Eukaryotic luciferase expression vector pTATALUC+, complete
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/note="splice and polyadenylation signals"
2078. .2094
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/db_xref="taxon:68900"
/plasmid="pTATALUC+"
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BioTechniques 23 (3), 436-438 (1997)
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/db_xref="GI:2598101"
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'note="polylinker"
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Altschmied, J. and Duschl, J.
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/gene="luc+"
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AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCGG 53
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1 (bases 1 to 416)

Rodaway, A., Takeda, H., Koshida, S., Broadbent, J., Price, B.,
Smith, J.C., Patient, R. and Holder, N.
Induction of the mesendoderm in the zebrafish germ ring by yolk
cell-derived TGF-beta family signals and discrimination of mesoderm
and endoderm by FGF
Development 126 (14), 3067-3078 (1999)
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DWIIARAGYYGNYCEGSCPAYWAGVPGSASFHTAVVNQYRWRGMSPGSVNSCCIPTK
LSTMSMLYFDDEVNIVKRDVPNMIVECGGCEFIDDI"
107 113 9 99 4
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
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Danio rerio mRNA for activin beta B protein, partial.
                                                                                                                                                                                                 0.9%; Score 38; DB 6; Length 360; 100.0%; Pred. No. 1.1e-07; ive 0; Mismatches 0; Indels
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                                                                                                            /db_xref="taxon:32630"
/note="Promoter region of plasmid TK-luc"
103 c 103 g 66 t
Forman, B.M., Beard, R.L. and Chandraratna, R.A.
Methods for modulating fxr receptor activity
Patent: WO 0076533-A 9 21-DEC-2000;
Allergan Sales, Inc. (US)
                                                                                                                                                                                                                                                                                     42 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCGG 79
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/protein_id="CAB43092.1"
/db_xref="G1:4867811"
                                                                                1. .360
/organism="synthetic construct"
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/gene="activin beta B"
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                                               Sales, Inc. (US)
Location/Qualifiers
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Smith, J.C.
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Best Local Similarity 100.
Matches 38; Conservative
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Best Local Similarity 100.
Matches 38; Conservative
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1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCGG 38

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    PAT 02-DEC-1994
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Actinomycetales: Corynebacterineae; Mycobacterium.
Mycobacterium. Mycobacterium tuberculosis complex.

E 1 (bases 1 to 2442)

McKendree, W.L.

Direct Submission

L Submitted (08-JUL-1997) McKendree W.L., Subtropical Insects

Research Management Unit, United States Horticultural Research

Laboratory, 2120 Camden Road, Florida, 32803, USA

E 2 (bases 1 to 2442)

S McKendree, W.L., Schuster, S.M. and Richards, N.

Structure of a recombinant glmS protein from Mycobacterium

tuberculosis expressed in E. coli
                                                                                                                                                                                                                 HALOARYLNITRILE DEGRADING GENE, ITS USE, AND CELLS CONTAINING THE GENE
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    linear
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    .2442
/organism="Mycobacterium tuberculosis"
/db_xref="taxon:1773"

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                                                                                                                                                                                                                                                                                     Patent: WO 8900193-A 1 12-JAN-1989;
109132 1195 bp
Sequence 1 from Patent WO 8900193.
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/db_xref="G1:2275059"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38;
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1. .1195
/organism="unknown"
a 335 c 330 g
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/transl_table=11
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/gene="glmS"
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polyA_signal
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BLCAT2DNA
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SSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVSFTSFDLNV
ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                                                                                                                               KAKVLAICNTNGSQIPRECDAVLYTRAGPEIGVASTKTFLÄQIAANYLLGLALAQARĞ
TKYDEVEREKEKHELEANPULARVIAARGPVAELAHRAQSSYVLELGSYVLELGHYGYEVALE
GALKIKELAYBHAGERAGELKHGPTALIEOGLPVIVWPSPKGSATLHAKLLSNIRE
IQTRGAVTIVIAEEGDETVRPYADHLIEIPAVSTLLQPLLSTIPLQVFAASVARARGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNCATBLB 4404 bp DNA linear SYN 16-FEB-1994 Cloning vector pBLCAT5 encoding thymidine kinase promoter and chloramphenicol acetyltransferase (CAT) and beta-lactamase genes,
                                         RPGRVWI PARRYGSPGNGWMGDGVRAVGNGRPVGGGSHPPNR I EVGNORDPVHREERH
OTPPTNEOVYGLRRLVRRFALLARPGDHVGALLPQDORTRVPDELQLVLGIWVGGVLA
                                                                                                  DSSG1ALVDGGTLTVRRRAGRLANLEEAVAEMPSTALSGTTGLGHTRWATHGRPTDRN
AHPHRDAAGKIAVVHNGIIENFAVLRRELETAGVEFASDTDTEVAAHLVARAYRHGET
                                                                                                                                                                    FIEHTREAVELGQDQAVVITADGYRISDFDGNDGLQAGRDFRPFHIDWDLAAAEKGGY
EYFMLKEIAEQPAAVADTLLGHFVGGRIVLDEQRLSDQELREIDKVFVVACGTAYHSG
LLAKYAIEHWTRLPVEVELASEFRYRDPVLDRSTLVVAISQSGETADTLEAVRHAKEQ
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                                                                                                                                              ADDFVGSVLAVLRRLEGHFTLVFANADDPGTLVAARRSTPLVLGIGDNEMFVGSDVAA
                     /translation="MTMITPSLHACRSTLEDPGHPSTLAVTWRMGPVGPRRTVPVTQS
                                                                                   FRARWPNSTIASVGRRDCPTDHAALPWSAVCGIVGYVGRRPAYVVVMDALRRMEYRGY
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Reporter constructs with low background activity utilizing the cat
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAT vector; beta-lactamase; chloramphenicol acetyltransferase;
thymidine kinase promoter; transient transfection vector.
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/note="SV40 polyadenylation signal"
complement(3038. 3898)
/gene="bla"
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                                                                                                                                                                                                                                                                                                                                                                                                    0.9%; Score 38; DB 1; 1
100.0%; Pred. No. 1.1e-07,
iive 0; Mismatches 0
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/db_xref="GI:208102"
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92184107
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38; Conservative
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/product="chloramphenicol acetyltransferase"
/protein_id="CAA45754.1"
/db_xref="G1:58161"
/translation="MEKKITGYTYVDISQWHRKEHFEAFQSVAQCTYVQTVQLDITAF
LKTVKKNKHKFYPAFIHILARLANNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETF
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                                                                                                                                                                                                                                               DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATWDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYN 26-FEB-1992
                                                                                                                                                                                             . ELDLNSGKILESFRPEERPPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
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                                                                                                                                                                   /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
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Neuenheimer Feld 280, W-6900 Heidelberg, FRG
2 (bases 1 to 4496)
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K6410
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/note="Herpes simplex virus tk promoter"
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EIGASLIKHW
4030. .4164
/note="SV40 polyadenylation signal"
4161. .4401
/note="SV40 polyadenylation signal"
-infs c 976 g 1227 t
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Pred. No. 1e-07;
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                                                                                                  /product="beta-lactamase"
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/organism="synthetic cor/db_xref="taxon:32630"
429. .598
                                                                                                                     /protein_id="AAA73139.1"
/db_xref="GI:455366"
complement(3038. .3898)
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/transl_table=11
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640. 1200
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1 (bases 1 to 4496)
Luckow, B. H. R.
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Best Local Similarity 100.
Matches 38; Conservative
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Local Similarity
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                                                                                                                                                                                                                            IELDLNSGKILLESFRPEËRFPMMSTFKVLLCGAVLSRIDAGGEOLGRRIHYSONDLVE
SPVETKHLTDOMTVRELCSAAITMSDNTAANLLTTTGGORFELTAFEINGDHYTRL
DRWEPELNEAI ENDERDTTWPWAMTILKLIJGELLTASROOLIDWMENVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSOATMDERNRQIA
                                                                                                                                                            /product-"beta-lactamase"
/protein_id="CAA45755.1"
/db_xref="81:58162"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF027128 4711 bp DNA circular SYN 08-NOV-1997
Eukaryotic luciferase expression vector ptkLUC+, complete sequence.
AF027128
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APANDIYNERELLNSMGISQPTVVFVSKKGLQKILNVQKKLPIIQKIIIMDSKTDYQG
SSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVSFTSFDLNV
               ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression vector ptkLUC+ artificial sequences: vectors.

1 (bases 1 to 4711)

Altschmied,J. and Duschl,J.
Set of optimized luciferase reporter gene plasmids compatible with widely used CAT vectors
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps,
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Direct Submission
Submitted (26-SEP-1997) Physiological Chemistry I/Biocenter,
University of Muerzburg, Am Hubland, Wuerzburg 97074, Germany
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                               Length 4496;
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                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 38; DB 12; ilarity 100.0%; Pred. No. 1e-07; Conservative 0; Mismatches 0
                                            1389. .2002
/note="SV40 small T intron"
1999. .2239
/note="SV40 signals"
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'note="polylinker"
                                                                                                                                                /transl_table=11
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/gene="luc+"
238. 1890
/gene="luc+"
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nes 38; Conserv
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KEYWORDS
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IELDLNSGKILLESFRPEERFPMMSTFKVLLCGAVLSRIDAGGEGLGRRIHÝSONDLVE
SPVTEKHLTDOMTVRELCSAAITWENDTAANLLTTIGGREITAFHUNGDHYTRL
DRWEPELNEAI DYNDERDTYMEYAFARTILRKLTGELLTASROQLIDWMESVAGFL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSOATWDERNRQIA
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Direct Submission
Submitted (27-001-1998) Department of Biochemistry, Stockholm
University, Svante Arrhenius vag. 10-12, Stockholm SE-10691, Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF102233 7055 bp. DNA circular SYN 24-NOV-1998
Transposon delivery vector pUTkml, complete sequence.
AF102233
FSHARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVLMYRFEEELFLRS
LQDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIASGGAPLSKEVGEAVAKRFHLP
                                              GIRQCYGLTETTSAILITPEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGVNQRGELCV
RGPMIMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGYQVA
PAELESILLQHPNIFDAGVAGLPDDDAGELPAAVVVLEHGKTMTEKEIVDYVASQVTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
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Mini-Tn5 transposon derivatives for insertion mutagene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4711;
                                                                                                                   AKKLRGGVVFVDEVPKGLTGKLDARKIREILIKAKKGGKIAV"
1922. .2143
/note="splice and polyadenylation signals"
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91035272
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Pred. No. 1e-07;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                   /product="beta-lactamase"
/protein_id="AABB3992.1"
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Transposon delivery vector pUTkml
                                                                                                                                                                                                                                             complement(3345. .4205)
                                                                                                                                                                                                                                                                                      complement(3345. .4205)
/gene="bla"
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complement(311. .1171)
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1 (bases 1 to 7055)
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1. .7055
                                                                                                                                                                                             2146. .2162
/note="polylinker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Scu.
100.0%; Pre
0;
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                                                                                                                                                                                                                                                                       /gene="bla
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/translation="wmeknikhsonfitskhnidkimtniklnehdnifeisskghf
teldykroptateisthkicktterklydhdhogylikklindfekroysyklydni
pynistdirklyedslanelylydygfakrilumtkslalilmabydislismypk
eyfhprpynynslirlsrkksrishkdrókynyfywkwynkeykkiftrnofnnslkh
                                                                                         EDEOSPEKITELYAECIRLEHSIDISCCPYTNSLDSRIAELDYLLNNDLADVDCENWE
EDTPPRDPRELYDFLKTEKPEEELVFSHGDLGDSNIFVKDGKVSGFIDLGRSGRADKW
YDIAFCVRSIREDIGEEQYVELFFDLLGIKPDWEKIKYYILLDELF"
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HPSVIIWSLGNESGHGANHDALYRWIKSVDPSRPVQYEGGGADTTATDIICPMYARVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQFFQFRLSGQTTEVTSEYLFRHSDNELLHWMVALDGKPLASGEVPLDVAPQGKQLIE
LPELPQPESAGQLWLTVRVVQPNATAMSEAGHISAWQQWRLAENLSVTLPAASHAIPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTTSEMDFCIELGNKRWQFNRQSGFLSQMWIGDKKQLLTPLRDQFTRAPLDNDIGVSE
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YRIDGSGQMAITVDVEVASDTPHPARIGLNCQLAQVAERVNWLGLGPQENYPDRLTAA
CFDRWDLPLSDMYTPYVFPSENGLRCGTRELNYGPHOWRGDFQFNISRYSQQQLMETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAIKNTKARNFGFLLYPDSIPNDWKEKLESLGVSMAVSPLHDMD
EKKDKDTWNSSDVIRNGKHYKKPHYHVIYIARNPVTIESVRNKIKRKLGNSSVAHVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDY IKGSYEYLTHESKDAIAKNKHIYDKKDILNINDFDIDRYITLDESQKRELKNLLL
DIVDDYNLVNTKDLMAFIRLRGAEFGILNTNDVKDIVSTNSSAFRLWFEGNYQCGYRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mTmITDSLAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEEAR
TDRPSQQLRSLNGEWRFAWFPAPEAVPESWLECDLPEADTVVVPSNWQMHGYDAPIYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYGQDSRLPSEFDLSAFLRAGENRLAVMVLRWSDGSYLEDQDMWRMSGIFRDVSLLHK
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                                                  /translation="MAKMRISPELKKLIEKYRCVKDTEGMSPAKVYKLVGENENLYLK
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                                                                         MTDSRYKGTTYDVEREKDMMLWLEGKLPVPKVLHFERHDGWSNLLMSEADGVLCSEEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="replication protein RepA"/protein_id="AAD46058.1"
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7335. .8069
                                                                                                                                                                                                                                                                                                                                                                                                                              /product="beta-d-galactosidase"
/protein_id="AAD46057.1"
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/protein_id="AAD46059.1"
/db_xref="G1:5668899"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(5425. .6123)
/gene="repA"
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                                                                                                                                                                        1090. .4520
/note="trp-lac2 fusion"
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                                                                                                                                                                                                                                                                                                       'note="promoterless"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:5668897
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/gene="lac2"
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/gene="emrC"
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GKTAFQVLEEYPDSGENIVDALAVFLRRLHSIPVCNCPFNSDRVFRLAQAQSRMNNGL
VDASDFDDERNGWPVEQVWKEMHKLLPFSPDSVVTHGDFSLDNLIFDEGKLIGCIDVG
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     /db_xref="G1:3907624"
/translation="MSIOHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
                                                  IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVDAGQEQLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
                                                                                                    DRWEPELNEAIPNDERDTTMPAAMATTLRKLLTGELLTLASRQOLIDWMEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                               /product-"kanamycin resistance protein"
protein_id="AAC79083.1"
/db_xref="GI:3907625"
/translation="MSHIORETSCSRPRLNSNMDADLYGYKWARDNVGQSGATIYRLY
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/product="3', 5'-aminoglycoside phosphotransferase type
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Vriesema,A.J.M., Brinkman,R., Kok,J., Dankert,J. and Zaat,S.A.J.
Direct Submission
Submitted (02-JUL-1998) Medical Microbia
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/notea-noiginates from Escherichia coli transposon Tn5"
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1 (bases 1 to 8142)

Vriesema,A.J., Brinkman,R., Kok,J., Dankert,J. and Zaat,S.A.

Broad-host-range shuttle vectors for screening of regulated promoter activity in viridans group streptococci: isolation of pH-regulated promoter.
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/db_xref="taxon:79020"
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Direct Submission
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This vector can be obtained from CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA. To place an order call (415) 424-8222 or (800) 662-2566, extension 1. International customers, please contact your local distributor. For technical information, call (415) 424-822 or (800) 662-2566, extension 3. This sequence has been compiled from information in the sequence databases, published literature and other sources, together with partial sequences obtained by CLONTECH; this vector has not been completely sequenced. If you suspect there is an error in this sequence, please contact CLONTECH; Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or E-mail
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/db_xref="taxon:31805"
2596 c 3033 g 2422 t
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Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 38; Conservative 0; Mismatches 0.
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Kitts, P.A.
CLONTECH Vectors On Disc version 1.3
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ORIGIN
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TITLE
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AUTHORS
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AUTHORS
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Submitted (07-02T-1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA Lambda DR2 can be obtained from CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA. To place an order call (415) 424-8222 or (800) 662-2566, extension 1. International customers, please contact your local distributor. For technical information, call (415) 424-822 or (800) 662-2566, extension 3. This sequence was compiled by Andrew Murphy and revised at CLONTECH. If you suspect there is an error in this sequence, please contact CLONTECH. Technical Service Department at (415) 424-822 or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.
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                                                                                                                    2 (bases I to 10850)
Murphy, A.J., Kung, A.L., Swirski, R.A. and Schimke, R.T.
cDNA expression cloning in human cells using the plambdaDR2
episomal vector system
Methods: A Companion to Methods in Enzymology 4, 111-131 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Cloning vector rpDR2"
/db_xref="taxon:31858"
/note="plasmid released from lambda DR2"
a 2615 c 3053 g 2459 t
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                                                                       CLONTECH Vectors On Disc version 1.3
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/db_xref="taxon:32630"
20 c 25 g
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synthetic construct
artificial sequences.
    Location/Qualifiers
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artificial sequences;
1 (bases 1 to 10850)
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DNA sequence of Ad S-adenosylmethioni vector plasmid pcM prEP78/52 hybrid a plasmid pcM prEP78/52 hybrid a plasmid pwR83196 e Commercial plasmid mMP9 promoter beta matrix metalloprot bNA sequence of pl Shuttle vector pAd Eukaryotic express vector pAPEX.3. S Shuttle vector pAD Capture DNA oligom Stabliser sequenc Bombyx mori R2 ele pUC18 polylinker (Phasmid pUC18 mult Cloning vector pHK Plasmid pEC2.0 mu Mutant cre pools p Streptavidin/prote NUR allele Recombinase enzyme Recombinase enzyme SaC; Hindill regio Multicloning site Potato virus X alp Milamol8(+) univers Synthetic plasmid

10 37 0.9 586 18 AAT58564 11 37 0.9 586 20 AAX00468 12 37 0.9 3796 21 AAA27831 13 37 0.9 4910 17 AAT15287	14 37 0.9 6295 19 AAV02043 15 37 0.9 7164 22 AAD10238 16 37 0.9 7380 20 AAX84028 17 37 0.9 7383 22 AAS00153 18 37 0.9 7612 21 AAS30529 19 37 0.9 7897 17 AAT27555	37 0.9 8540 16 AAT08476 37 0.9 8540 17 AAT41900 37 0.9 8932 20 AAX19816 37 0.9 8932 21 AAA07342	24 37 0.9 9972 17 AAP72557 Shuttle vec 25 37 0.9 19307 17 AAP727558 Shuttle vec 26 36 0.9 40 18 AAP46199 Capture DNC	36 0.9 50 16 AAQ96167 36 0.9 50 24 ABL51437 36 0.9 57 13 AAQ5617	30 36 0.9 59 21 31 36 0.9 59 22 32 35 0.9 59 22 32 35 0.9 59 22 35 35 0.9 59 59 22 35 35 0.9 50 50 50 50 50 50 50 50 50 50 50 50 50	33 36 0.9 60 22 AAF74634 34 36 0.9 60 24 ABA99032 35 36 0.9 63 21 AAC63087	36 0.9 66 15 AAQ66558 36 0.9 66 24 ABL59115	36 0.9 72 17 36 0.9 72 17 36 0.9 72 17	36 0.9 72 18 AA765088 Sac_L HindIIII 36 0.9 72 21 AA299200 Multicloning 36 0.9 74 14 AAQ3737 Potato virus 36 0.9 74 15 AA64588 MISIND 8(+) use 36 0.9 75 24 ABK86942 Synthetic pl	ALIGNMENTS	RESULT 1 AAA97430 ID AAA97430 standard; DNA; 4115 BP.	AAA97430;	Z9-JAN-Z001 (iirst entry)	XX XX Execution dehydrogenase; SLDH; L-sorbose production; NADP+ dependent; KW D-sorbitol; mannitol; arabitol; oxidation; 2-keto-L-gluconic acid; XW L-ascorbic acid biosynthesis; vitamin C; ds.	OS Gluconobacter oxydans.		16-MAR-2000; 20	PR 17-MAR-1999; 99JP-0072810. PR 06-AUG-1999; 99JP-0224679. XX PA (FUJI) FUJISAWA PHARM CO LTD.	PI Shibata T, Ichikawa C, Matsuura M, Noguchi Y, Saito Y; PI Yamashita M, Takata Y; XX DX WPI: 2000-587530/55. DR P-PSDB; AAB23172.
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: May 19, 2003, 01:52:01; Search time 844 Seconds (without alignments) 10979.826 Million cell updates/sec	Title: US-09-926-163B-1 Perfect score: 4115 Sequence: 1 aagcttgcatgcatgcaggttccgggcggcctgaagctt 4115	Scoring table: OLIGO_NUC Gapop 60.0 , Gapext 60.0	Searched: 2185239 seqs, 1125999159 residues	Word size : 0 Total number of hits satisfying chosen parameters: 4370478	um DB seq length: 0 um DB seq length: 2000000000	Post-processing: Listing first 45 summaries	Database : N_Geneseq_101002:* 1: /SIDS2/qcqdata/qeneseq/qeneseqn-embl/NA1980.DAT:*	2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:* 3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:* 4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:* 5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:* 6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:* 7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*	/ SIDSZ/gcgdata/geneseq/yeneseqn embl/Mrison.brit. 8: /SIDSZ/gcgdata/geneseq/geneseqn-embl/Mrison.brit.* 9: /SIDSZ/gcgdata/geneseq/geneseqn-embl/Mrisos.brit.* 10: /SIDSZ/gcgdata/geneseq/geneseqn-embl/Mrisos.brit.* 11: /SIDSZ/gcgdata/geneseq/geneseqn-embl/Mrisos.brit.*	12: /SIDSZ/gcgdata/geneseq.embl/NA1991.DAT:* 13: /SIDSZ/gcgdata/geneseq.geneseqn.embl/NA1991.DAT:* 14: /SIDSZ/gcgdata/geneseq/geneseqn.embl/NA1992.DAT:* 14: /SIDSZ/gcgdata/geneseq/geneseqn.embl/NA1993.DAT:*		10: /SIDSZ/gcgdata/genesed/genesegn-embL/NA199/.DAT:* 19: /SIDSZ/gcgdata/geneseg/genesegn-embL/NA1998/DAT:* 20: /SIDSZ/gcgdata/geneseg-genesept-batts/	21: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:* 22: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:* 23: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:* 23: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:* 24: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed,	SUMMARIES	Result Query No. Score Match Length DB ID Description	4115 100.0 4115 21 AAA97430 38 0.9 1195 10 AAN91189 37 0.9 92 12 AAQ11697 37 0.9 116 21 AAQ11690	5 37 0.9 586 12 AAQ1823 Region of pUG19-SA 5 37 0.9 586 15 AAQ78008 Bacteriophage T3 S 7 0.9 586 15 AAQ78008 Bacteriophage T3 S 8 16 17 AAQ87073 Bacteriophage T3 S 8 18 37 0.9 586 17 AAT09985 S-adenosylmethioni 9 37 0.9 586 17 AAT09964

culturing its gene-transformed host cells, useful for producing L-sorbose or 2-keto-L-gluconic acid as an intermediate in L-ascorbic acid production obtainable derived D-sorbitol dehydrogenase oxydans Gluconobacter

9; Page 60-63; 72pp; Japanese Claim The invention relates to Gluconobacter oxydans D-sorbitol dehydrogenase (SLDH; AAB21172) and to the gene encoding it (AAA97430). SLDH has a molecular weight of about 54 kba and catalyses the conversion of D-sorbitol into L-sorbose using NADP+ as a co-enzyme. SLDH specifically catalyses the oxidation of sorbitol, mannitol and arabitol, but does not encompasses expression vectors and placerol. The invention also encompasses expression vectors and host cells comprising the cluconobacter oxydans SLDH gene, and the recombinant production of SLDH. The invention further relates to a method for preparing L-sorbose by contacting the recombinant SLDH with D-sorbitol; a process for producing 2-keto-L-gluconic acid by contacting recombinantly produced sorbose dehydrogenase and/or sorbosone dehydrogenase with L-sorbose; and a process for preparing L-ascorbic acid or its alkaline earth metals salts by conversion from 2-keto-L- gluconic acid. SLDH is useful for producing L-sorbose or 2-keto-L- gluconic acid as an intermediate in L-ascorbic production. The present sequence represents the Gluconobacter SLDH gene. acid

Sequence 4115 BP; 833 A; 1133 C; 1270 G; 879 T; 0 other;

ö 240 240 540 120 180 180 300 300 360 360 420 420 480 480 900 9 9 1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCGGTTTTGGCAGCGCTCCCTAGATT GACCGGGAACACAGGCCTGCTGCTTTGTACAAGGGGCTGAGTCATGCGCTGCGTGGGCT GGCACATAGTTGCGAAGAGCAGTTGCGCGCAAAGCAGAACCAGCATGAACAGCAGTCCGA GCCACATAGTTGCGGAGGAGCAGTTGCGCGCAAAGCAGAACCAGCATGAACAGCAGTCCGA AGACGAGGAAATCCTCGGCCTCCTACCGCGATTGGAAGAGCAGACCCGTCCTGAGATGCG TTTTGTGATGTCCCTGTTCCGCGAGGATCTCGAACGGGCTGTTGGGGGTGCTCATGCGTTC TGATGCGAGTGCCGCAAAAGGTCTCTGAACAGGACGTCCCGCGGAGGGCAGTCAGAGGTC GAAATGGCTCCTGTTGAAACCGTCATTCGGTTTTTACGTTGTTTCGGGGCTATGATGGCA CATGCCCGGCCTTGTCGGTCCCCGTCAGCGCCCCGAAACCACGGGGAGAATTCCATGA TTACGCGCGAAACCCTTAAGTCTCTTCCTGCCAATGTCCAGGCTCCCCCCTATGACATCG ACGGGATCAAGCCTGGGATCGTGCATTTCGGTGTAGGTAACTTTTTTCGAGCCCATGAGG Gaps 4115; ; 0 Length Indels 21; ; 0 DB Score 4115; Pred. No. 0; Mismatches 0; 100.0%; 100.0%; Conservative Best Local Similarity Matches 4115; Conserv 61 19 241 361 481 541 601 Query Match 121 121 181 181 301 361 421 421 481 301 õ g ò Вb ò qq οy QQ ò Оþ δ Ω QY qq οy g Qγ og οy q ŏ

1440 1740 1020 1080 1500 1680 780 780 840 840 900 900 960 960 GTGACTATCTGCTTGCCCCGGCCGATCCGGAAGCCGTGCTGAAGCATCTTGTTGTTGATCCGG AGGTGTTCTGGACGGAACCGTGCGTCGAGGACGAAGCGGGACCTGTCACGTA ATTCCCTGACCGAGACGGCTCCGTCCGGCAAGAGCACGGTGCGCGTCATGGGCGCGCTGC GTGACTATCTGCCTCGGCCGGATCCGGAAGCCGTGCTGAAGCATCTTGTTGATCCGG CCATCCGCATCGTTTCCATGACGATCACGGAAGGCGGCTACAACATCAACGAGACGACGG GTGCGTTCGATCTGGAGAATGCGGCAGTAAAGGCCGACCTCAAGAACCCGGAAAAGCCGT CTACCGTTTTCGGTTACGTGGTCGAGGCCCTGCGTCGTTGGGATGCCGGTGGTAAGG CATTTACGGTCATGTCCTGTGATAACCTGCGTCATAACGGCAATGTCGCCCGCAAGGCCT TCCTCGGCTATGCGAAGGCGCGCGCGATCCGGAGTTGCCGAAGTGGATTGAGGAAAACGCGA CCTTCCCGAACGGAATGGTTGATCGCATCACCCCGACCGTTTCGGCGGAAATCGCCAAGA AGTGGGTGCTGGAAGACCAGTTTGCGGATGGCCGTCCGCCGCTTGAAAAAGCCCGCGTGC AGATGGTCGGGGACGTGACGGACTGGGAGTACGTCAAGATCCGAATGCTCAATGCAGGGC ATGTCATGCTCTGCTTCCCAGGCATTCTGGTCGGCTATGAGAATGTGGATGACGCCATTG AAGACAGCGAACTCCTTGGCAATCTGAAGAACTATCTCAACAAGGATGTCCTGGACCC TGAAGGCGCCTTCAGGCATGACGCTCGAAGGCTATCGGGACAGCGTCATCAGCCGTTTCT CCAACAAGGCGATGTCGGACCAGACGCTCCGGATTGCTAGCGATGGCTGTTCCAAGGTTC TGACGGGCAGTGACCGTTCAAAGAAAAAAGCCGAGGAATTCAAGGCCCAGGACTGCCTGT CGTTCTACGTCGAGCAGATTCTTGAACACGCTCCGGACTGGGCGATTGTTGGTGGTCTTGGCC 1021 1081 1321 1141 1201 1261 1261 1441 1141 1201 1321 1381 1381 1441 1561 1681 661 661 721 721 781 781 841 841 901 901 196 961 1021 1081 1501 1501 1561 1621 1621 601 qq Db g g g Db qq qq g qq g δ Op q g qq ò Qγ δy ò οy ${}_{Q}^{\chi}$ δλ g qq ò ٥y ò $^{\circ}$ οy òγ Óγ οy οy ò

KESULT 2 AAN91189

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This is a fragment of the regulatable expression vector, pWH332 which comprises two tet-operators ol and O2 and three tet-promoters A, R1 and R2, in addition to the tet A / cat gene fusion. It is used in the construction of the regulatable expression vectors pWH353 and pWH354 which comprise (a)the retracycline repressor gene (tetR): (b) a Bacillus adapted tetR-promoter sequence: (c) an adapted xylose-isomerase promoter sequence (xylp); and (d) at least one tet-operator sequence (tetO) between the consensus regions of proteins in Bacillus hosts. See also AAQ11698-700.
                                                                     Plasmid pWH332 fragment comprising tetracycline A/ cat gene fusion
                                                                                                                     Tetracycline repressor; tetR promoter; xylose-isomerase promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vector for inducible protein over-expression in Bacillus - ha
tetracycline repressor gene and its adapted promoter, xylose
isomerase promoter and tetracycline operator sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pJL6; produce; vector; sequence; clone; expression;
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Pred. No. 4.3e-07
0; Mismatches 0
                                                                                                                                                                                                                                                                                       90..92
/*tag= b
/label= fragment of cat gene
                                                                                                                                                                                                                                                a
tetracycline A gene
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                                                                                                                                                                                          Location/Qualifiers
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100.0%; Pro
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AAA10800/c
ID AAA10800 standard; DNA; 116
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                       (first entry)
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/label=
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Matches 37; Conserv
                                                                                                                                               ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MERE ) MERCK
                                                                                                                                                  tet-operator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-2000
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                       19-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA10800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                  misc_RNA
                                                                                                                                                                                                                                                                                            misc_RNA
  NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                             4080
CATCAGGGTCCGGATCACTCAGCAGCTCCCGCGCAGAAGATATAAGCGACGGATCGGCCG 3960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified nitrilase gene (nit-23) carried on plasmid pBrx23 has 17 AAs cpUC19 replacing its 5' truncated terminus. It can be incorporated into E.coli or plants, providing protection from bromoxynil and related herbicides, and allowing decoxification of contaminated areas.
                            AGTTGCCGATCGCGATCAGGACAGTTACGTACGAACCGGTTGCGTTCCGTTTGACC
                                                                                                                                                                                                GGAGAGCCAGAAAAAACGTCCGGAATGTCGCATTATCCAGCCGCACCAGTTCGTCGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifiled nitrilase gene (nit-23) carried on plasmid construct pBrx23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pure modified bacterial nitrilase and gene - used for detoxifying environments and protecting hosts from bromoxynil and related herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1195 BP; 294 A; 335 C; 331 G; 235 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nitrilase; benzonitrile; bromoxynil; detoxification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCGG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                        TTTGGTGCAATCAGCTCCGGGCGGGCCTGAAGCTT 4115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; L 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Scor.
100.0%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN91189 standard; DNA; 1195 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klebsiella pneumoniae ozaenae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RHON ) RHONE POULENC AGROC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88WO-EP00588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; ; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
AAQ11697/c
ID AAQ11697 standard; DNA; 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1989-039649/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAP94259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO8900193-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stalker D;
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3901
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Length 92;

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Tomato E8 promoter; transgenic fruit; ethylene production inhibition; S-adenosylmethionine hydrolase; delayed fruit ripening; ds.
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                                                                                                                                          Control of ethylene biosynthesis in plants - by introducing gene which encodes S-adenosyl methionine hydrolase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic fruit-bearing plants, esp. tomato – contg. exogenous gene under control of E8 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriophage T3 SAM-K modified S-adenosylmethionine hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 586 BP; 144 A; 146 C; 157 G; 139 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score 37; DB 12; L
Pred. No. 3.9e-07;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 AAGCTIGCATGCCTGCAGGTCGACTCTAGAGGATCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualiflers
66..524
        Brown L;
                                                                                                                                                                                                                                  Disclosure; Fig 6; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ78008 standard; DNA; 586 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.
Matches 37; Conservative
     Ferro AJ, Bestwich RK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                          WPI; 1991-208140/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIT-) EPITOPE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-341873/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also AAQ11822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage T3
                                                                                        P-PSDB; AAR12520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR74824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bestwick RK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9424294-A
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AAQ78008
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (i) a promoter for controlling exogenous gene transcription;
(ii) a reverse sequencing primer sequence;
(iii) an RBS (ribosome binding site) sequence and SD sequence;
(iv) a multiple cloning site directly downstream of the SD sequence;
(v) a positive sequencing primer sequence;
(vi) a terminator for controlling exogenous gene termination.
The multiple cloning site contains the enzymic incision site of a blunt end type restriction endonuclease, and the interval of SD-AUG is 5-8 multiple cloning, and the expression of exogenous genes in the molecular biology field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the nucleotide sequence of pJL6. The invention relates to methods for producing a vector containing the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                            vector, and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                         Generation, cloning and sequence determination of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                  (HUAC-) HUACHEN BIOLOGICAL TECH RES INST SHANGHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 116 BP; 32 A; 24 C; 28 G; 32 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

0.9%; Score 37; DB 21; 1
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/label= AdoMetase
                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 3; 16pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region of pUC19-SAM-K vector
                                                       98CN-0116333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ11823 standard; DNA; 586
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                                                                                                             98CN-0116333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homoserine; MTA; ss.
                                                                                                                                                                                                                                                                               WPI; 2000-351200/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage T3
                                                     17-JUL-1998;
                                                                                                          17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-DEC-1990;
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26-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                       use thereof
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RESULT 5 AAQ11823

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Length 586; Indels

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Best Local Similarity 100.
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                      W09535387 + A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  27-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-1995
                                                                                                                                     AAT09985;
                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                          RESULT 8
                                                                                                     AAT0998
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                    AAQ78007 the tomato E8 gene promoter, and AAQ78008 which encodes AAR74824 the bacteriophage T3 derived SAM-K modified S-adenoslymethionine hydrolase (AdoMetase), were used in the construction of a vector. The vector was used to produce transgenic tomato plants which expressed AdoMetase under the translational control of the E8 promoter. AdoMetase is an inhibitor of ethylene production, and therefore an inhibitor of fruit ripening.
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This DNA encodes an S-adenosylmethionine-hydrolase enzyme which hydrolyzes SAM to homoserine and S'-methylthioadenosine. A transgenic plant containing this sequence displays reduced ethlyene blosynthesis resulting in fruits, vegetables and flowers with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reducing ethylene biosynthesis in plants - by introducing DNA encoding a S-adenosylmethionine-hydrolase enzyme into a plant host.
                                                                                                                                                                                                                                                                                                                                                  Bacteriophage T3; phage T3; S-adenosylmethionine-hydrolase; AdoMetase; SAM-hydrolase; enzyme; senescence; ethylene; hormone; shelf-life; preservation; ripening; fruit; flower; plasmid pUC19SAM-K; ss.
                                                                                                                                                           ö
                                                                                                                                   Query Match 0.9%; Score 37; DB 15; Length 586; Best Local Similarity 100.0%; Pred. No. 3.9e-07; Matches 37; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 586 BP; 144 A; 146 C; 157 G; 139 T; 0 other;
                                                                                                               Sequence 586 BP; 144 A; 146 C; 157 G; 139 T; 0 other;
                                                                                                                                                                                                                                                                                                                                Bacteriophage T3 S-adenosylmethionine-hydrolase gene.
                                                                                                                                                                                            24 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 60
                                                                                                                                                                                1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          improved shelf life and preservation qualities
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
66..522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferro AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig. 6; 16pp; English.
Claim 18; Fig 11; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90US-0613858.
94US-0255833.
                                                                                                                                                                                                                                                             AAQ87073 standard; DNA; 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-0448095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89US-0448095
                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bestwick RK, Brown LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AGRI-) AGRITOPE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-193491/25.
                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriophage T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR75212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-1989;
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                                                                                                                                                                                                                                                                                                        20-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5416250-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-DEC-1989;
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                                                                                                                                                                                                                                                                                   AAQ87073;
                                                                                                                                                                                                                                        RESULT 7
                                                                                                                                                                                                                                                   AAQ87073
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Length

Score 37; DB 16;

Query Match

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                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic plants with modified ripening phenotype - contg. a chimeric gene contg. a sequence which encodes a prod. which reduces ethylene biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a modified S-adenosylmethionine-hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a //note= "Region modified by linker to contain a eukaryotic translation initiation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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100.0%; Pred. No. 3.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-adenosylmethionine-hydrolase; phage T3; chimeric gene; tomato; E4 promoter; E8 promoter; fruit; transgenic plant; ripening; ethylene; tissue-specific gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= S-adenosylmethionine-hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 586 BP; 144 A; 146 C; 157 G; 139 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-adenosylmethionine-hydrolase gene from pUC19-SAM-K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and a subsequent reduction in ethylene biosynthesis
                                                                                                                  24 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 60
                                                                                 1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
Pred No. 3.9e-07;
0; Mismatches 0;
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Mismatches
                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 88-89; 139pp; English.
                                                                                                                                                                                                                                                                                             AAT09985 standard; cDNA to mRNA; 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage T3 (ATCC 11303-B3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ferro AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . . 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  improvement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR88611
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BP

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AdoMetase; bacteriophage T3; ethylene biosynthesis; transformation; S-adenosylmethionine hydrolase; hydrolysis; S-adenosylmethionine; AdoMet; homoserine; S'-methylthioadenosine; MTA; ornamentel plant; l-aminocyolopropane-1-carboxylic acid; ACC; inhibitor; ACC synthase; transgenic plant; fruit; vegetable; flower; shelf life; preservation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Control of ethylene biosynthesis in plants using vector encoding
                                                                DNA sequence of AdoMetase gene with modified 5' end.
AAT58564 standard; DNA; 586
                                                                                                                                                                                                                                                                                                                                                                                  (AGRI-) AGRITOPE INC
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-076910/07
                                                                                                                                                                  Bacteriophage T3.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAW11594
                                                                                                                                                                                                                                                                                                                                                                                                        RK,
                                                                                                                                                                                                                                                                                                    12-DEC-1989;
                                                                                                                                                                                                                                                                                                                                    12-DEC-1989;
08-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                           20-DEC-1994;
                                          17-SEP-1997
                                                                                                                                                                                                                                                        US5589623-A
                                                                                                                                                                                                                                                                                                                           12-DEC-1990;
                                                                                                                                                                                                                                                                               31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                        Bestwick
                                                                                                                                              food;
 The coding sequence of the phage T3 S-adenosylmethionine hydrolase gene was altered (AAT09964) so that the endoded enzyme, designated SAM-K (AAR88601), had an isoleucine to valine substin at position efficiency of the gene in plants. Transgenic raspberry and strawberry plants carrying the altered gene (see also AAT09967) were obtd. using a high-efficiency transformation and regeneration system. They, showed reduced levels of ethylene biosynthesis in leaf tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic red raspberry and strawberry plants - produce fruit with increased sugar content, increased fungal or viral resistance, or
                                                                                                                                                                                       S-adenosyl cleaving enzyme; SAMase; raspberry; Rubus idaeus;
stravberry; Fragaria ananassa; transgenic plant; fruit rot;
disease resistance; fungus resistance; virus resistance; ethylene;
ripening; crop improvement; ds.
                                                                                                                                                                             S-adenosylmethionine hydrolase; AdoMet hydrolase; AdoMetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 586 BP; 144 A; 146 C; 157 G; 139 T; 0 other;
        AACCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 37; DB 17; I
100.0%; Pred. No. 3.9e-07;
                                                                                                                                                       S-adenosylmethionine hydrolase SAM-K cDNA.
                                                                                      ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 42-43; 85pp; English.
                                                                                      AAT09964 standard; cDNA to mRNA; 586
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mathews HV;
                                                                                                                                                                                                                                                                  Location/Qualifiers
66..523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reduced ethylene biosynthesis
                                                                                                                                                                                                                                                                                                                                                          95WO-US07753
                                                                                                                                                                                                                                                                                                                                                                               95US-0384556
                                                                                                                                                                                                                                                                                                                                                                                           94US-0263900
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferro AJ,
                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                (EPIT-) EPITOPE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-058425/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR88601
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bestwick RK,
                                                                                                                                                                                                                                                                                                               WO9535388-A1
                                                                                                                                                                                                                                                                                                                                                          16-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                 3-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-1994;
                                                                                                                                13-MAY-1996
                                                                                                                                                                                                                                                                                                                                     28-DEC-1995
                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fruit
                                                                                                          AAT09964;
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                                                                                                                                                                                                                                                                  Key
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Ferro AJ;

Brown LR,

90US-0613858. 89US-0448095. 94US-0255833. 94US-0360974.

89US-0448095

Location/Qualifiers 66..524 /*tag= a /product= AdoMetase

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This sequence represents the AdoMetase gene derived from bacteriophage T3. This sequence may be used in the method of the invention to control ethylene biosynthesis in plants. This is done by transforming plant cells with a vector which contains a DNA sequence (I) allowing genetic selection in plant cells and a DNA sequence (II) allowing genetic selection in plant cells and a DNA sequence (II) encoding S-adenosylmethionine hydrolase (AdoMetase (AdoMetase) which hydrolyses S-adenosylmethionine (II) are flanked by regulatory elements that allow expression in plant cells. AdoMetase reduces levels of AdoMet, the essential precursor of ethylene (via 1-aminocyclopropane-1-carboxylic acid (ACC)) and MTA is an inhibitor of AcC synthase, the major enzyme involved in ethylene (synthasis. Transgenic plants containing this construct produce fruits, vegetables and flowers of improved shelf life and preservation qualities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A wide range of food and ornamental plants can be modified. The transgenic plants are able to control ethylene production under restricted conditions. This sequence has been modified around the
       flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 586;
S-adenosyl:methionine hydrolase - used to produce fruit, etc. of increased shelf life and preservation quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transgenic plants are able to control ethylene productic restricted conditions. This sequence has been modified initiation codon to produce an optimised Kozak sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 586 BP; 144 A; 146 C; 157 G; 139 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.9e-07;
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Mismatches
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                                                                                                          Example 3; Fig 6; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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Gaps

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Indels

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100.0%; Prec. ...

Local Similarity 100. nes 37; Conservative

Best Loca Matches

AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 60 1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37

RESULT 10 AAT58564

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AAX00468;

RESULT 11 AAX00468

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Key

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The present sequence is that of eukaryotic expression vector plasmid pcWn-McI. The plasmid is derived from pcWnbeta by replacing the Lac2 coding sequence with a linker containing multiple restriction sites. Modification of the human cytomegalovitus (CW) immediate early promoter was accomplished by substituting the sequence between SacI and the 2nd NotI site of pcMv-McI with a synthetic linker. North American porcine reproductive and respiratory syndrome (PRRS) virus P129A cDNA (see AAA27809) was cloned into the modified vector to create pcMv-S-P129 (ATCC 203489), which was used to demonstrate cellular expression of PRRS virus by direct transfection of cDNA into call a spanies. The invention relates to polynucleotide molecules, plasmids, viral vectors and transfected host cells that comprise North American
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide encoding an infectious RNA molecule of a North American porcine reproductive and respiratory syndrome virus for use a vaccine in protecting swine and other animals from infection by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRRS DNA. It also relates to polynucleotide molecules, viral vectors and transfected host cells encoding a genetically modified North American PRRS virus that is disabled in its ability to cause
                                                                                                                                                                      North American PRRS virus; Nidovirales virus; pig; swine; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRRS, or which encodes 1 or more heterologous antigenic epitopes,
                                                                                                                                                                                                                               Chimeric - Porcine reproductive and respiratory syndrome virus. Chimeric - Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%; Score 37; DB 21; Length 3796; 100.0%; Pred. No. 3.5e-07; ve 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3796 BP; 953 A; 934 C; 956 G; 953 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 43-44; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sheppard MG;
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100.08; Pit
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  AAA27831 standard; DNA; 3796 BP.
                                                                                                                                                                                                                                                                                                                                                                                    99EP-0309409.
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Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PFIZ ) PFIZER PROD INC
                                                                                                                              Vector plasmid pCMV-MC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Welch SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-444364/39.
                                                                                                                                                                                            pCMV-S-P129;
                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-1999;
                                                                                                                                                                                                                                                                                                EP1018557-A2
                                                                                                                                                                                                                                                                                                                                                                                                                              22-DEC-1998;
                                                                                  12-SEP-2000
                                                                                                                                                                                                                                                                                                                                            12-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calvert JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogen -
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                                          AAA27831;
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AAT15287
    δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  containing a DNA sequence encoding S-adenosylmethionine hydrolase (SAMase) linked to a promoter selected from a group consisting of: (a) a tomato E4 promoter; (b) a tomato E8 promoter; and (c) an avocado cellulase promoter; (d) a tomato E4 promoter/SAMase construct. Expression from the promoter is induced during fruit ripening optionally by ethylene synthesised in the fruit. The SAMase transgene produces fruit with reduced ethylene synthesis, delaying fruit ripening and lengthening storage periods. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                          Ethylene; plant hormone; regulator; metabolism; senescence; E4; E8; S-adenosylmethionine hydrolase; SAMase; promoter; fruit ripening; storage; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic plants containing S-adenosylmethionine hydrolase gene - useful for delaying fruit ripening and lengthening storage periods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a transgenic fruit-bearing plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 586 BP; 144 A; 146 C; 157 G; 139 T; 0 other;
24 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. 3.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified SAMase gene from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                    S-adenosylmethionine hydrolase modified gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.9%; Score 37; DB
100.0%; Pred. No. 3.9
                                                                                                        AAX00468 standard; cDNA to mRNA; 586 BP
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
66..524
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 11; 72pp; English.
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94US-0255833.
94US-0261677.
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90US-0613858
                                                                                                                                                                                          (first entry)
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Best Local Similarity 100.
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bestwick RK, Ferro AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIT-) EPITOPE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-120030/10.
                                                                                                                                                                                                                                                                                                                                                         Bacteriophage t3.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW30604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-OCT-1994;
                                                                                                                                                                                          31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5859330-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-1989;
12-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-OCT-1994
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virus for use as

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27-OCT-1996 (first entry)

RESULT 12 AAA27831/c

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/*tag=
                                                                                                                                                          (AURA-) AURAGEN INC.
                                                                                                                                                                                                 WPI; 1998-041898/04.
                                                                                                                                                                                                            P-PSDB; AAW44004-05
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es 37; Conserv
                                                                                                                  04-JUN-1997;
                                                                                                                                      05-JUN-1996;
                                                                        W09746263-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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            intron
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                               CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                          Hybrid adenovirus-adeno-associated virus for gene therapy - comprises adenovirus portion, 5' and 3' ITR sequences from AAV and a
                              reporter gene; transgene; somatic gene therapy; gene transfer; plasmid prEP78/52; familial hypercholesterolemia; cystic fibrosis;
                                                                                                                                                                                                                                                                                                      This cDNA encodes recombinant plasmid pRep78/52, a trans-acting plasmid containing the AAV sequences that encode rep 78 kD and 52 kD proteins under the control of the AAV P5 promoter. The plasmid also contains an SV40 polyadenylation signal. This cDNA is used in the construction of a hybrid AAV-AV virus vector. The hybrid virus may be used in the delivery and stable integration of a selected gene into the chromosome of a target cell, i.e. gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-12; IL-12; cytokine; growth factor; mousel
plasmid pWRG3196; cancer; tumour; metastasis; gene therapy; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                therapy of cystic fibrosis and familial hypercholesterolaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 37; DB 17; Length 4910;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4910 BP; 1161 A; 1294 C; 1215 G; 1240 T; 0 other;
                   Adeno virus; adeno-associated virus; hybrid virus vector;
prEP78/52 hybrid adeno virus-adeno-associated virus cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 3.4e-07; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pWRG3196 encoding murine interleukin-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhesus macaque polyoma virus
                                                                                                                                                                                                                                                                                   Disclosure; Page 57-61; 91pp; English.
                                                                                                                                                                                                                                                              selected trans:gene, e.g. CFTR or LDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encephalomyocarditis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= p35 subunit
                                                                       Adeno virus; Adeno-associated virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                 Wilson JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV02043 standard; DNA; 6295 BP
                                                                                                                                      95WO-US14018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytomegalovirus.
Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                             (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              955..1675
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                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Mus musculus
                                                                                                                                                                                                 Fisher KJ, Kelley WM,
                                                                                                                                                                                                                     WPI; 1996-239504/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyclic; circular.
                                                                                                                                  27-0CT-1995;
                                                                                           WO9613598-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric - C
Chimeric - B
Chimeric - R
Chimeric - e
                                                                                                                09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV02043;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Plasmid pWRG3196 is a bicistronic plasmid encoding both subunits,
i.e. p35 (see AAW44004) and p40 (see AAW44005), of murine interleukin-12
(IL-12). The p35 and p40 subunits were cloned from a mouse spleen
CIL-12). The p35 and p40 subunits were cloned from a mouse spleen
CIL-12). The p35 and p40 subunits a single cytomegalovirus promoter,
an SV40 splicing donor/splicing acceptor, and bovine growth hormone
polyA signal. Between the p35 and p40 genes is an internal
ribosome entry site element (IRES) cloned from encephalomyocarditis
virus. The backbone of the plasmid is from pUC19. Plasmid
pWRG3139 induces about half the expression of IL-12 as the tandem
vector pWRG3136 (see AAV02042) in vivo and in vitro. A novel method
of treating tumours in a mammal involves delivering copies of an
expressible foreign genetic construct, especially pWRG3169 or
pWRG3196, comprising a promoter operative in the mammalian
cepidermal cells and DNA sequences encoding p35 and p40 subunits of
IL-12 to target cells in vivo. Delivery of the construct allows
IL-12 expression for treatment of solid metastatic or disseminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid; cyclic; circular; replicon; exogenous gene; marker gene; transcription termination; immunostimulatory sequence; ISS; antiviral; non-essential nuclectide; molecular biology application; gene therapy; DNA vaccine; cloning; gene expression; in vitro protein production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-12 gene therapy of tumours – comprises delivering construct containing promoter and sequences encoding interleukin-12 p35 and p40 subunit(s) to target cells in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumours, and regression of established tumours. The treatme effective even when the genetic construct is delivered to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6295 BP; 1610 A; 1610 C; 1568 G; 1507 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
/note= "contains an intron" 1261..1333
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                                                                                                                                                                                                   /product= p40 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Commercial plasmid vector pCMVbeta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 33-38; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.9%; Sccilarity 100.0%; Pr
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US09591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rakhmilevich AL, Yang N;
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promoter, intron, exgenous gene, transcription termination sequence, selectable marker gene, detectable marker gene and an immunostimulatory sequence (ISS), where the non-essential nucleotide sequences have been substantially removed from these vectors. The plasmid DNA vectors are useful in most molecular biology applications, e.g. gene therapy, DNA vaccines, cloning and expression of genes, and in the in vitro production of polypeptides and/or proteins. The present sequence is a commercial plasmid DNA vector pCMVbeta which comprises Cytomegalovirus promoter, simian virus 40 (SV40) intron, the lacz gene, pUC origin of replication and the ampicillin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "5' non-coding region of lacz gene from pUC18 that corresponds to the non-essential nucleotide sequence that have been removed in the novel DNA plasmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                            non-essential nuclectide sequence that have been removed in the novel DNA plasmid vector. 7007.7164
/*tag= c /*tag= c /non-coding region of lac2 qene from DUC18 that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to plasmid DNA vectors comprising essentially of a replicon and at least one other component selected from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New plasmid DNA vectors, useful for most molecular biology applications, e.g. gene therapy, DNA vaccines, cloning and expression of genes, and in the in vitro production of polypeptides and/or proteins.
                                                                                                                                                                                                                              /*tag= a
/note= "Corresponds to the non-essential nucleotide
sequence that have been removed in the novel DNA
plasmid vector"
4513.4890
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/note= "pUC18 lac2 promoter that corresponds to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7164;
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cytostatic; pCMVbeta; cytomegalovirus promoter; lac2 gene; ampicillin gene; simian virus 40; SV40 intron; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 37; DB 22; Length 71
100.0%; Pred. No. 3.3e-07;
tive 0; Mismatches 0; Indels
                                                                            Chimeric - Cytomegalovirus.
Chimeric - Rhesus macaque polyoma virus.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 42-44; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIM-) ELIM BIOPHARMACEUTICALS INC.
                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-2001; 2001WO-US01255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-2000; 2000US-0480879
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Best Local Similarity 100.
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-451855/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200151626-A2.
                                                                                                                                                                                   Key
misc_feature
                                                                                                                                                                                                                                                                                                                                             misc_feature
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Job time: 872 secs

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28 36 0.9 5 2 31 36 0.9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	0.000000000000000000000000000000000000		43 36 0.9 44 36 0.9 45 36 0.9			RESULT 1 US-08-046-583-10 ; Sequence 10, Application	2 2			; ZIP: 94306 ; COMPUTER READABLE FORM	COMPUTER: FLOPPY COMPUTER: IBM PC CO	; SOFTWARE: Patentin ; CURRENT APPLICATION DA' ; APPLICATION NUMBER:	; FILING DATE: 09-APR; CLASSIFICATION: 800	NAME: Fabian, Gary REGISTRATION NUMBER:	REFERENCE/DOCKET NUM	; TELEPHONE: (415) 32-	; INFORMATION FOR SEQ ID NG SEQUENCE CHARACTERISTIC	LENGTH: 586 base pa		HYPOTHETICAL: CDNA CO ANTI-SENSE: NO	; ORIGINAL SOURCE: ; INDIVIDUAL ISOLATE: . FFAMILIE.	; DAME/KEY: CDS ; LOCATION: 66521 US-08-046-583-10
GenCore v Copyright (c) 1993 -	OM nucieic - nucieic search, using sw model Run on: May 18, 2003, 22:35:30 ; Search time 178 Seconds (without alignments) 7089.746 Million cell updates/sec	-163B-1 catgcctgcagġt	Scoring table: OLIGO_NUC Gapop 60.0 , Gapext 60.0 .	0 :	Total number of hits satisfying chosen parameters: 882724	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Listing first 45 summaries	<pre>Database : Issued_Patents_Nh:* 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:* 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:* 3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:* 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:* 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:* 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*</pre>	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No Score Match Length DB ID Description	37 0.9 586 1 US-08-046-583-10 Sequence 10 37 0.9 586 1 US-08-384-556A-1 Sequence 1,	37 0.9 586 2 US-08-331-355A-22 Sequence 37 0.9 586 5 PCT-1US94-12364-22 Sequence 37 0.9 586 5 PCT-1US95-07753-1 Sequence	37 0.9 4910 2 US-08-331-384-2 Sequence 2, 37 0.9 4910 2 US-08-836-087-2 Sequence 2,	37 0.9 4910 4 US-09-246-320-2 Sequence 2, 37 0.9 4910 4 US-09-546-738-2 Sequence 2,	37 0.9 6295 2 US-08-659-206A-4 Sequence 4, 37 0.9 7897 3 US-08-836-022A-1 Sequence 1,	12 37 0.9 7897 4 US-09-427-048A-1 Sequence 1, 13 37 0.9 8540 4 US-08-487-283A-4 Sequence 4,	37 0.9 8540 5 PCT-0S95-05611A-12 Sequence 12, 37 0.9 8932 2 US-08-252-493C-8 Sequence 8, 37 0 8833 2 US-08-257-493C-8	10 37 0.9 9972 3 US-09-270-17-0 Sequence 17 37 0.9 9972 3 US-09-686-022A-3 Sequence 18 37 0.9 9972 4 US-09-477-048A-3 Sequence	37 0.9 19307 3 US-08-836-022A-10 Sequence 10, 37 0.9 19307 4 US-09-427-048A-10 Sequence 10,	36 0.9 40 36 0.9 50 36 0.9 50	24 36 0.9 57 1 05-08-089-910-19 Sequence 22, 25 36 0.9 57 1 08-089-910-22 Sequence 22, 26 36 0.9 57 1 08-08-400-864-4 Sequence 4, 27 36 0.9 57 4 08-09-116-492A-33 Sequence 33.

Sequence 1, Appli	Patent No. 5166321	Sequence 66, Appl	Sequence 8, Appli	Sequence 5, Appli	8, 7	Patent No. 5304637	Patent No. 5166321			Sequence 73, Appl	Sequence 1, Appli.	Sequence 3, Appli	Sequence 1, Appli	Patent No. 5231168	Sequence 6, Appli	Sequence 7, Appli	Sequence 11, Appl
US-09-233-507-1	5166321-2	US-08-261-206A-66	US-09-586-935-8	US-08-470-369-5	US-09-214-146-8	5304637-5	5166321-4	US-08-484-956-73	US-08-757-653-73	US-08-520-946-73	US-07-729-460A-1	US-08-422-613-3	US-07-780-717C-1	5231168-15	US-08-373-134D-6	US-08-373-134D-7	US-08-585-585A-11
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36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36
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ALIGNMENTS

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US-08-046-583-10

IS-GRUERAL 10. Application US/08046583

Requence 10. Application US/08046583

Requence 10. Application US/08046583

Retart No. 527346

Retart No. 527346

REPLICANT BESTAICH, Richard K

APPLICANT RETO. Adolph J Transgenic Tomatoes Expressing TITLE OF INVENTION: Reduced Ethylene Synthesis and Delayed TITLE OF INVENTION: S-Adenosylmethionine Hydrolase CORRESPONDENCE ADDRESS: 12

CORRESPONDENCE ADDRESS: 12

CONFRYE: Tabla Alco Acompatible CONFRY: 1350

CONFRYE: RADALE FORM: STREE: Floppy disk COMPUTER: Inhe Compatible CONFRY: 1406

CONFRYER: Paland Alco CONFRY: 1006

SOFTWARE: Paland CAPPE: 1009

CONFRYER: Paland CAPPE: 1009

CONFRYER: Paland CAPPE: 1009

CONFRYER: Paland CAPPE: 1009

ATTORNEY APPLICATION UNIVERS: 33475

REGISTRATION UNIVERS: 33475

RECIENAL: (415) 324-0960

INCORMATION FOR SEQ ID NO: 100: 100

SEQUENCE CHARACTERISTICS: 100

CERRENAL: 100 ANT: SEQ ID NO: 100

SEQUENCE CHARACTERISTICS: 100

CENTRAL SOURCE: Unear MOLECULE TYPE: NO MARE: FEBRE ON MARE: PEBRE ON MARE: PEBR
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APPLICANT: Ferro, Adolph J
TITLE OF INVENTION: Regulated Expression of Heterologous
TITLE OF INVENTION: Genes in Plants and Transgenic Fruit
TITLE OF INVENTION: with a Modified Ripening Phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,355A
                                                                                                                                                                                                                      ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,677
FILING DATE: 17-UNN-1994
PRIOR: APPLICATION DATA:
APPLICATION NUMBER: US 08/046,583
FILING DATE: 09-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/255,833
FILING DATE: 08-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 448,095
FILING DATE: 12-DEC-1989
ATTORNEY AGENT INFORMATION:
NAME: Evans, Susan T: 8443
REGISTRANTION NUMBER: 4257-001
TELECOMMUNICATION INFORMATION:
Sequence 22, Application US/08331355A Patent No. 5859330 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                     Bestwick, Richard K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 44
                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                  Palo Alto
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                                                                                                                                                                                                                                                                                                                              94306
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US-08-331-355A-22
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                                                                     APPLICANT:
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        0.9%; Score 37; DB 1; Length 586; 100.0%; Pred. No. 2.6e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        APPLICANT: Mathews, Helena V
APPLICANT: Bestwick, Richard K
APPLICANT: Bestwick, Richard K
APPLICANT: Bestwick, Adolph J
TITLE OF INVENTION: Plant Genetic Transformation
TITLE OF INVENTION: Methods and Transgenic Plants
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,556A
                                                                                                                   24 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCG 60
                                                                                             1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33,875
R: 4257-0010.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/263,900
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                            Sequence 1, Application US/08384556A
Patent No. 5750870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 586 base pairs
TYPE: nucleic acid
           Query Match 0.99
Best Local Similarity 100.
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palo Alto
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
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US 07/613,858

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                                                                                                                                                                                                                                                                                                                 24 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 60
                                                                                                                                                                                                                                                                                                  1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                             Score 37; DB 2; Lo
Pred. No. 2.6e-07;
                                                                                                                                                               Fig. 11, pUC19-SAM-K
                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                     0.9%; Scc.
100.0%; Pre
0;
                                                                                                        MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
(415) 324-0880
           TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2
                                                       586 base pairs
                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                         Conservative
                                                                   nucleic acid
                                                                                                                                                                 INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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RESULT

24 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 60

В

RESULT 3 US-08-331-355A-22

1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37

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APPLICANT: Wilson, James M.
APPLICANT: Kelley, William M.
APPLICANT: Kisher, Krishna J.
TITLE OF INVENTION: Hybrid Adenovirus-AAV Vector and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/NR/22
                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 5; L
Pred. No. 2.6e-07;
                                                                                                                                                                                 PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/384,556
FILING DATE: 03-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/263,900
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4257-0010.41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

Query Match

O.9%; Score 37; DB

Best Local Similarity 100.0%; Pred. No. 2.6

Matches 37; Conservative 0; Mismatches
                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/08331384
; Patent No. 5856152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 324-0880
TELEFRAX: (415) 324-0860
INFORMATION FOR SEO 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE: SAM-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 586 base pairs
TYPE: nucleic acid
                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE
                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION:
PCT-US95-07753-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-331-384-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
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                                                                            TITLE OF INVENTION: Regulated Expression of Heterologous TITLE OF INVENTION: Genes in Plants and Transgenic Fruit TITLE OF INVENTION: with a Modified Ripening Phenotype NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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Methods and Transgenic Plants
                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 AAGCTIGCAIGCCTGCAGGTCGACTCTAGAGGATCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Le 2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE-DOCKET NUMBER: 4257-0011.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig. 11, pUC19-SAM-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Plant Genetic Transfor TITLE OF INVENTION: Methods and Transgenic NUMBER OF SEQUENCES: 11
CORRESONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                   E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,677
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
                 Sequence 22, Application PC/TUS9412364
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application PC/TUS9507753 GENERAL INFORMATION:
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100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
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MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                           ZIP: 94306
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.9
Best Local Similarity 100.
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 66..521
                                                                                                                                                                                                                             Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                      ADDRESSEE:
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PCT-US94-12364-22
PCT-US94-12364-22
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                                                                                                                                                                                                                                                                       COUNTRY:
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                                                           APPLICANT:
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STATE:
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Length 4910;
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                                                                                                                                                                                                                                                                                                                                               Krishna J. Hybrid Adenovirus-AAV Vector and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 AAGCTTGCATGCCTGCAGTCGACTCTAGAGGATCG 435
                                                                                                                                                                                                                                                                    Trustees of University of Pennsylvania
                                                                                                            399 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 435
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                                                                                      1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
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Pred. No. 2.1e-07;
0; Mismatches 0;
          Score 37; DB 2; LA Pred. No. 2.1e-07;
0.9%; Scc.
100.0%; Pred. No. 2...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Methods of Use Thereof
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100.0%; Pre
0;
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                                                                                                                                                                                                      US-09-246-320-2; Sequence 2, Application US/09246320; Patent No. 6251677
                                                                                                                                                                                                                                                                                                                       APPLICANT: Kelley, William M.
APPLICANT: Fisher, Krishna J.
TITLE OF INVENTION: Hybrid Aden
TITLE OF INVENTION: Methods of
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bak, Mary E. REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4910 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.99
Best Local Similarity 100.0
Matches 37; Conservative
            Query Match 0.9%
Best Local Similarity 100.(
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spring House
Pennsylvania
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT:
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US-09-546-738-2
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                                                                                                                                                                                                                                                                                                                                                   Length 4910;
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TITLE OF INVENTION: Hybrid Adenovirus-AAV Vector and
TITLE OF INVENTION: Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                 399 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trustees of University of Pennsylvania
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,087
                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                               0.9%; Score 37; DB 2; L
100.0%; Pred. No. 2.1e-07;
tive 0; Mismatches 0;
              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UPNG1149USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,384
FILING DATE: 28-007-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08836087
Patent No. 5871982
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson, James M.
Kelley, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,21.
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                            LENGTH: 4910 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.8
Matches 37; Conservative
                                                                                                                                                      TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennsylvania
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                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: CDNA
US-08-331-384-2
                                                                                                                                                                                                                                                                      unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE:
US-08-836-087-2
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                                                                                                                                                                                                                                                                        TOPOLOGY:
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APPLICANT:
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STATE:
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Length 6295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3666 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 3630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: join(955..1260, 1334..1675)
OTHER INFORMATION: /product= "p35 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 2377..3384
COTHER INFORMATION: /product= "p40 gene product"
US-08-659-206A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,022A
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                                                                                                                                                                                                                                                                                               TOPOLOGY: circular MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "plasmid pWRG3196"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,215
REFERENCE/POCKET NUMBER: GNVPN.008PCT
FELECOMMUNICATION INFORMATION:
TELECHONE: 215-540-9200
                                                                                          110229.91144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/331,381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                             NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 6295 base pairs
                                                                                                                                                          TELEFAX: 608-251-9166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                             LENGTH: 6295 base pai
TYPE: nucleic acid
STRANDEDNESS: double
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ADDRESSEE: Howson an
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COUNTRY: USA
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  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
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100.0%; Pred. No. 2.1e-07;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,738
FILING DATE: 11.Apr-2000
CLASSIFICATION: CUNKNOWN>
                                          TITLE OF INVENTION: Hybrid Adenovirus-AAV Vector and Methods of Use Thereof
                                                                                                                                                          STREET: Spring House Corporate Cntr, PO Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rakhmilevich, Alexander
TITLE OF INVENTION: IL-12 Gene Therapy of Tumors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: GNVPN. 007PCT

TELECOMMUNICATION INFORMATION:

TELEFAX: 215-540-9200

TELEFAX: 215-540-5818

INFORMATION FOR SEO ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/246,320 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: undrown

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-546-738-2
                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/659,206A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08659206A
Patent No. 5922685
Kelley, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4910 base pairs
                     Krishna J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     STATE: Pennsylvania
                                                                                                                                                                               CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 37; Conservative
                                                                                       NUMBER OF SEQUENCES:
                       Fisher,
                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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US-08-659-206A-4/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: WI
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Gaps

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609 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 645

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INFORMATION FOR SEQ ID NO:

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Gaps
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VENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
VENTION: OF INFLAMMATORY DISEASES
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Pred. No. 2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seth A. Fidel.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-152.1 CIP
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: 3.5 inch, 1.4Mb storage
Macintosh Cetris 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/487,283A FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/236,208
FILING DATE: 02-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application PC/TUS9605611A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    E: Seth A. Fidel
25 Science Park (Alexion)
                                                                                                                                     Evans, Mark J.
Matis, Louis A.
Mueller, Eileen Elliott
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apex-3P Eukaryotic
                                                                              Sequence 4, Application US/08487283A Patent No. 6355245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expression Vector
                                                                                                                                                                                                                                                   Springhorn, Jeremy P. Squinto, Stephen P. Thomas, Thomas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Lenardo. Michael J.
McFarland, Henry F.
                                                                                                                                                                                                                                     Rother, Russell P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8540 base pairs
                                                                                                                                                                                                Nye, Steven H.
Rollins, Scott
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                         New Haven
Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Circular
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
.....hes 37; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                    ; Patent No. 6355245
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                           RESULT 13
US-08-487-283A-4/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06511
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APPLICANT:
APPLICANT:
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                                                                                                                                                        0.9%; Score 37; DB 3; Length 7897;
100.0%; Pred. No. 2e-07;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7897;
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Trustees of the University of Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Spring House Corporate Cntr, P O Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2e-07;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MURBRE: US/09/427,048A
FILING DATE: 21-OCt-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Improved Adenovirus Virus and Methods of Use Thereof
                                                                                                                                                                                                                                                     609 AAGCTTGCATGCTGCAGGTCGACTCTAGAGGATCCG 645
                                                                                                                                                                                                                                 1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GNVPN.008PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 37; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/836,022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09427048A Patent No. 6203975 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson, James M.
Fisher, Krishna J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen, Shu-Jen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
SEQUENCE CHARACTERISTICS:
LENGTH: 7897 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.9°
Best Local Similarity 100°.
Matches 37; Conservative
                                                                                                                                                      Query Match 0.9
Best Local Similarity 100.
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                        STRANDEDNESS: doul
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
US-08-836-022A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF
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                                                                                                                                                                                                                                                                                                                         RESULT 12
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MEDIUM TYPE: 3.5 inch, 750 Kb storage COMPUTER: PC compatible OPERATING SYSTEM: DOS 6.2
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: May 19, 2003, 01:51:55 Job time: 235 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apex-3 Eukaryotic
Expression Vector
                                                                                                                       SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/:
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (203) 776-1790
TELEFAX: (203) 772-3655
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  June 1, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8932 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 8932 base pai
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
                                                                                                                                                                                                              FILING DATE: June 1,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
    Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESCRIPTION:
DESCRIPTION:
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                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                       APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1371 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 1335
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                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Wats, Mark J.
APPLICANT: Matis, Louis A.
ITITLE OF INVENTION: PORCINE E-SELECTIN
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/POCKET NUMBER: 30,399
REFERENCE/POCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERIST
Matis, Louis A.
Mueller, Eileen Elliott
Nye, Steven H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
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Apex-3P Eukaryotic
Expression Vector
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STREET: 25 Science Park, Box 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08252493C
Patent No. 5891645
                                                                                                                                                                                        Maurice M. Klee
                                                                                                                                                                                                            1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 8540 base pairs
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Klee, Maurice M. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Double
                                                                                                                                                                                                                                  CITY: Fairfield
STATE: Connecticut
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DESCRIPTION:
DESCRIPTION:
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                                                                                                                                                                                        ADDRESSEE:
STREET: 19
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                                          APPLICANT
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  Length 8932;
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Query Match 0.9%; Score 37; DB 2; Le Best Local Similarity 100.0%; Pred. No. 2e-07; Matches 37; Conservative 0; Mismatches 0;
                                                                                                  1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCG 37
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Sequence 32, Appl Sequence 161, App Sequence 1, Appl Sequence 3, Appl Sequence 73, Appl Sequence 8, Appl Sequence 6, Appl Sequence 6, Appl Sequence 11, Appl Sequence 106, App Sequence 106, App Sequence 106, App Sequence 267, App Sequence 267, App Sequence 267, App
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Sequence 162, App
Sequence 5, Appli
                                                                                              ; Search time 457 Seconds
  (without alignments)
11615.089 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-10-021-237-5
US-09-940-9258-73
US-09-785-269-8
US-09-380-932-3
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US-09-777-564-106
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US-09-940-925A-162
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US-09-973-013-6
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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Match Length DB
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Maximum I
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Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 16, Appl
Sequence 11, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 15, Appl
Sequence 18, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 26, Appl
Sequence 18, Sppl
Sequence 18, Sppl
Sequence 26, Appl
Sequence 26, Appl
Sequence 1873, Appl
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OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3796;
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US-09-757-992-13

US-09-78-7-992-13

US-10-132-561-14

US-10-132-561-13

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US-10-132-561-13

US-09-894-882-53

US-09-894-882-8
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US-09-940-925A-49
US-10-033-297-27
US-10-013-28-32
US-09-940-244-27
US-09-940-925A-32
US-09-940-925A-165
US-10-132-561-11
US-10-132-561-12
US-10-132-561-12
US-98-885-1244-4
US-98-885-1246-4
US-98-885-1246-4
US-09-885-157-6
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100.0%; Pred. No. 1.6e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                          US-09-764-847-1873
                                                                                                                                                                                                                                                                                                             .US-09-772-134B-26
US-09-772-134B-29
US-10-092-154-1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Plasmid:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 161, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION: APPLICANT: BROW, MARY ANN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/10127391
Patent No. US20020172690A1
GENERAL INFORMATION:
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4458
4459
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560
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586
586
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 32
LENGTH: 3796
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Best Local Similarity
Matches 37; Conserv
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ORGANISM: Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-127-391-32/c
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  FEATURE:
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Length 57;

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DB 10; L
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                                       REGISTRATION NUMBER: 31,024
REFERENCE/DOCKET NUMBER: 862.1335/WFH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2024341501
TELEFAX: 2024341501
                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 1
Pred. No. 7.26
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: USO 09/259,467
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: PCT/US98/09952
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 08/971,845
PRIOR FILING DATE: 1997-08-08
PRIOR FILING DATE: 1997-08-08
PRIOR FILING DATE: 1997-06-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%; Score 36; DB 100.0%; Pred. No. 7.2 ative 0; Mismatches
                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09939275A Patent No: US20020172955A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: template region US-09-939-275A-3
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Best Local Similarity 100.0%; P
Matches 36; Conservative 0;
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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Best Local Similarity
                                                                                                                                                                                                     LENGTH: 57
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TITLE OF INVENTION: METHOD AND APPARATUS FOR AUTOMATICALLY
REMOVING VECTOR UNIT IN DNA BASE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Staas & Halsey
STREET: 700 Eleventh Street, N.W., Suite 500
                                                                   ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/940,925A
FILING DAFE: 10-Jun-2002
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/684,674
FILING DATE: 22-JUL-1996
                                                                                                                                 STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA ZIP: 94104 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/785,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: RNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 161: US-09-940-925A-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: <Unknown>
    PATHOGENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                               CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: IMAI, Kensaku
                           SEQUENCES: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20001
COMPUTER READABLE FORM:
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                                                   CORRESPONDENCE ADDRESS
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                           NUMBER OF
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US-09-785-269-1
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APPLICANT: Adams, Christopher
APPLICANT: Boles, T. Christian
APPLICANT: Boles, T. Christian
APPLICANT: Welr, Lawrence
APPLICANT: Welr, Lawrence
APPLICANT: Summers, Nevin
TITLE OF INVENTION: Methods for Purifying DNA Using Immobilized Capture Probes
FILE REFERENCE: EXT-062CN
CURRENT APPLICATION NUMBER: US/09/939,275A
CURRENT FILING DATE: 2001-08-24
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7.2e-09;
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KITAJIMA, Masato
TITLE OF INVENTION: METHOD AND APPARATUS FOR AUTOMATICALLY
REMOVING VECTOR UNIT IN DNA BASE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,269
FILING DATE: 20-Feb-2001
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Staas & Halsey
STREET: 700 Eleventh Street, N.W., Suite 500
                                                 DB 9; Leus
7.2e-09;
0;
                                                                                                                                                   1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCC 36
                                                                                                                                                                           0.9%; Score 36; DB 10; 1
100.0%; Pred. No. 7.2e-09;
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REGISTRATION NUMBER: 31,024
REFERENCE/DOCKET NUMBER: 862.1335/WFH
                                                                 Score 36; DB 5
Pred. No. 7.2e-
8; Mismatches
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APPLICATION NUMBER: US 08/684,674
FILING DATE: 22-JUL-1996
        SEQUENCE DESCRIPTION: SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic); SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-09-785-269-8
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                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09785269
Patent No. US20020018736A1
GENERAL INFORMATION:
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, Sequence 3, Application US/09380932
; Patent No. US20020058250A1
; GENERAL INFORMATION:
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TELEFAX: 2024341501
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STRANDEDNESS: double
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                                                                 Query Match 0.9%;
Best Local Similarity 77.8%;
Matches 28; Conservative
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 36; Conservative
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                       US-09-940-925A-73
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                                    APPLICANT: Dhanda, Rahul
APPLICANT: Exton, Stephen
TITLE OF INVENTION: Purification Devices Comprising Immobilized Capture Probes and US
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
CURRENT APPLICATION NUMBER: US/10/021,237
CURRENT FILING DATE: 2001-12-06
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OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 59;
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Pred. No. 7.2e-09;
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100.0%; Pred. No. /...
0; Mismatches
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REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/940,925A FILING DATE: 10-Jun-2002 CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/513,381
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/121,836
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
LENGTH: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 73, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BROW, MARY ANN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: RNA (genomic)
Adams, Christopher
Boles, T. Christian
Dhanda, Rahul
Kron, Stephen
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: artificial sequence
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Best Local Similarity 100°.
Matches 36; Conservative
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Query Match
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APPLICANT: Ullmann, Agnes
TITLE OF INVENTION: BACTERIAL MULTI-HYBRID SYSTEM AND APPLICATIONS THEREDE
FILE REFERENCE: 0395.0195.019
CURRENT APPLICATION UMBER: US/09/955,649
CURRENT FILING DATE: 2000-08-01
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APPLICANT: Ladant, Daniel
APPLICANT: Ladant, Daniel
APPLICANT: Ladant, Agnes
APPLICANT: Williann, Agnes
TITLE OF INVENTION: BACTERIAL MULTI-HYBRID SYSTEM AND APPLICATIONS
TITLE OF INVENTION: THEREOF
FILE REPERENCE: 03495.0178
CURRENT APPLICATION NUMBER: US/09/972,985
CURRENT APPLICATION NUMBER: 09/203,681
PRIOR APPLICATION NUMBER: 09/203,681
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VOS: 2.1
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TITLE OF INVENTION: EXTRACTION AND UTILISATION OF UNTR ALLELES FILE REFERENCE: 28911/35930 CURRENT APPLICATION NUMBER: US/09/380,932
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100.0%; Pred. No. 7.1e-09;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. w..
                                                                  CURRENT FILING DATE: 1999-03-21
PRIOR APPLICATION NUMBER: PCT/GB98/00840
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: EP 97301917.7
PRIOR FILING DATE: 1997-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 36; Conservative
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Matches 36; Conservative
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APPLICANT: Ladant, Daniel
                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: genomic DNA
US-09-380-932-3
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US-09-972-985-6
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US-09-955-649-6
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LENGTH: 75
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LENGTH: 71
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APPLICANT: Kalimova, Gouzel
APPLICANT: Ulimann, Agnes
TITLE OF INVENTION: BACTERIAL MULTI-HYBRID SYSTEM AND APPLICATIONS THEREOF
FILE REFERENCE: 03495,013 602-01-09
CURRENT APPLICATION NUMBER: US,09/973,013
PRIOR PRICATION NUMBER: US,09/203,681
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 6
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
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                                                                                                                                                                                                                                                                                                                    0.9%; Score 36; DB 10; i
100.0%; Pred. No. 7.1e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 10;
Pred. No. 7.1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: The Secretary of State for Defence
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Mismatches
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APPLICANT: Vincent, Suzanne P
TITLE OF INVENTION: Amplification process
FILE REFERENCE: CG/P/133/WOD
CURRENT APPLICATION NUMBER: US/10/135,807
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: PCT/IB98/02085 PRIOR FILING DATE: 1998-12-04 NUMBER OF SEQ ID NOS: 11 SOFTWARE: PATENTIN VEr. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: GB 0110501.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/10135807 Publication No. US20030049655A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 36; Conservative
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Matches 36; Conserv
                                                                                                                                                                                                                             , NAME/KEY: CDS
; LOCATION: (1)..(75)
US-09-955-649-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
) LOCATION: (1)..(75)
US-09-973-013-6
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                                                                      SOFTWARE: Pat
SEQ ID NO 6
LENGTH: 75
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TOPOLOGY: unknown MOLECULE TYPE: cDNA
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                          ; OTHER INFORMAT
US-09-777-564-106
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                                                                                                                                                         Description of Artificial Sequence: Modified polylinker sequence of pTTQ18NHK
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Patent No. US20020022591A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION NO. US200301008299A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul OS21030108299A1
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493C1
CURRENT FILING DATE: 2002-03-02
NUMBER OF SEQ ID NOS: 1739
SOFTWARE: FastSEQ for Windows Version 4.0
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n. 7e-09;
0; Indels
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Best Local Similarity 100.0%; Pred. No. 7.1e-09;
Matches 36; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 7e-
Live 0; Mismatches
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CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: FastSEQ for Window Version 4.0
SEQ ID NO 106
LENGTH: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 106, Application US/10015219 Publication No. US20030008299A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: n = A,T,C or G
                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
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Best Local Similarity 100.
Matches 36; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                         OTHER INFORMATION: OTHER INFORMATION:
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US-09-777-564-106/c
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                                                                               LENGTH: 89
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David M. Lough
Guobing Xiang
TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
NUMBER OF SEQUENCES: 320
CORRESPONDENCE ADDRESS:
                                                                                                                                       ö
                                                                                            Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
                                                                                       DB 10; L
7e-09;
hes 0;
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FILING DATE: 06-NO. US20020042112A1-96
APPLICATION NUMBER: 08/744,481
FILING DATE: 06-NO. US20020042112A1-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/746,055
FILING DATE: 06-No. 0820020042112A1-96
APPLICATION NUMBER: 08/746,036
FILING DATE: 06-No. US20020042112A1-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2004B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/20444
FILING DATE: 06-NOV-1997
APPLICATION NUMBER: 08/947,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/179,536B
FILING DATE: 26-Oct-1998
                                                                                         0.9%; Score 36; DB 100.0%; Pred. No. 7e-tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 08-Oct-97
APPLICATION NUMBER: 08/933,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/786,988
FILING DATE: 23-Jan-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/787,639
                                                                                                                                                                                                                                                                                                                                               ; Sequence 267, Application US/09179536B
; Patent No. US20020042112A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seidman, Stephanie L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: ASCII
LOCATION: (1) \dots (102)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELEPHONE: 858-450-8400
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-Sep-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION
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ZIP: 92037
COMPUTER READABLE FORM:
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INFORMATION FOR SEQ ID NO:
                                                                                         Query Match 0.9
Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CA
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 267:
US-09-179-536B-267
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0; Gaps Query Match

0.9%; Score 36; DB 10; Length 103;
Best Local Similarity 100.0%; Pred. No. 7e-09;
Matches 36; Conservative 0; Mismatches 0; Indels ò qq

Search completed: May 19, 2003, 07:50:56 Job time: 461 secs

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Word size :

Searched:

Database :

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A1000514 CTT-HSP-2
B31188 HS-1007-A2-
B3121080 K-EST0089
Bm740520 K-EST0011
B31114 HS-1007-A1-
B9340 CTT-HSP-228
BM85023 K-EST0130
BM85023 K-EST0130
                                                                                                                                                                                                                                                       AQ002527 CIT-HSP-2
B34609 HS-1025-A1-
B32855 HS-1016-A1-
B41250 HS-103-A2-
BM851117 K-ESF0131
B32887 HS-1016-A1-
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B30702 HS-1003-A1-
B32593 HS-1015-B1-
AQ059544 CIT-HSP-2
BM852504 K-EST0133
B45032 HS-1060-B1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225777 241 bp mRNA linear EST 08.OCT-1998 phA-I-2R/LLW Outward Alu-primed hncDNA library Homo sapiens cDNA clone phA-I-2R/LLW, mRNA sequence.
                                      BM851683 K-EST0132
BM850221 K-EST0130
AL097303 Drosophil
B33347 HS-1017-A2-
                                                                                                                                                                                                                                                                                                                                       Bm852732 K EST0134
Bm850274 K-EST0130
B31778 HS-1012-B1-
Bm821456 K-EST0090
                                                                                                                                                                                                                AQ080154 CIT-HSP-2
AQ080152 CIT-HSP-2
B40812 HS-1052-B1-
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BM849662 K-EST0129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 241)
Vinogradova, T.V., Lebedev, Y.B., Kopantzev, E.P., Wagner, L.L., Volik, S.V., Ermolaeva, O.D., Lavrentyeva, I., Monastyrskaya, G.S. and Sverdlov, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                        Bm852441 K-EST0133
Bm747927 K-EST0022
                                                                                            AT000691 AT000691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structure and Function of Human Genes
Shemyakin Institute of Bioorganic Chemistry
16/10 Miklukho-Maklaya, Moscow, 117871, Russia
12-1 70953306529
Fax: 70953306538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: sverd@humgen.siobc.msk.su
B32178
B40882
B79682
BM851683
BM85021
CX500271
B3347
AT000691
AQ006733
BM821080
BM821080
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BM95340
BM85033
B38698
AQ080153
AQ08012
AQ00252
B34609
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BM85117
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BM821456
BM821148
BM849662
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BM852504
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BM850274
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BM747927
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1. .241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
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225777
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B60048 CIT-HSP-385
B70879 CIT-HSP-206
B70567 CIT-HSP-205
B64148 CIT-HSP-202
AQ916288 nbeb00630
                                                                                                       (without alignments)
12382.837 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                        1 aagcttgcatgcctgcaggt..........tccgggcgggcctgaagctt 4115
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                                                                                       May 19, 2003, 02:27:41; Search time 5382 Seconds
                                                                                                                                                                                                                                                                                                 32308132
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                         residues
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                                                                                                                                                                                                                                                                                                                                                                   summaries
                                                              nucleic search, using sw model
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B60048
B70879
B70567
B64148
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Gapop 60.0 , Gapext 60.0
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            /clone_lib="Outward_Alu-primed hncDNA library"
//note="Vector: pGEN-32; Site=1: EcoR1; Site_2: BamH1; The
/library was constructed as described in [Obradovic, D. V.
Borodin, A.M., Kopantzev, E.P., Wagner, L.L., Volik, S.V.,
Emclaeva, O.D., Lebedev, Y.B., Monastyrskaya, G.S.,
Sverdlov, E.D. (1993) Bloorganicheskaya khimia, 20,
919-930]. This protocol is based on nested primer strategy
using Alu- specific primers (ALN3 and TC-65) that direct
the hncDNA synthesis outward of Alu repeats."
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Seq primer: M13-21
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CIT-HSP-385K18.TFB CIT-HSP Homo sapiens genomic clone 385K18, DNA
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1 (bases 1 to 534)
Adms, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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ive 0; Mismatches 0;
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Pred. No. 1.3e-08;
0; Mismatches 0;
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/db_xref="GDB:5378802"
/db_xref="taxon:9606"
/clone="385x18"
/clone="1b="CIT-HSP"
/sex="Male"
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Other_GSSs: CIT-HSP-385K18.TRB
Contact: Mark Adams
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100.0%; Pre
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Best Local Similarity 100°
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B70879 11-GSS 21-JUN-1998
CIT-HSP-2063C19.TF CIT-HSP Homo sapiens genomic clone 2063C19, DNA
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Seq primer: M13-21
Class: BAC ends.
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1 (bases 1 to 617)
4 (bases 1 to 617)
7 (bases 1 to 617)
8 (bases 1 to 617)
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Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Building
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Clones are available from Research Genetics (info@resgen.com)
end search page:
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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1.2e-08;
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Other_GSSs: CIT-HSP-2063C19.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
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/db_xref="GDB:7061446"
/db_xref="taxon:9606"
/clone="2063C19"
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                                                                                                             Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Email: mdddams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
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Seg primer: M13-21
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Adams,M.D. Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden
'K., Berry.K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M.
and Venter,J.C.
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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hes 0; Indels
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Fax: 301 838 0208
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. 672
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GDB:7060128"
                                                                             Unpublished (1997)
Other_GSSs: CIT-HSP-2059L21.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="2059L21"
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B64148.1 GI:2638138
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Location/Qualifiers

FEATURES

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/note="Vector: pasterialists of the property of the world control of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 131 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza satura, Nipponbare variety using EcoRI as the cloning enzyme. The
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nbeb0063017f CUGI Rice BAC Library (ECORI) Oryza sativa genomic
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Mukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 763)
Ming, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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                                            /db_xref="cDB:7045354"
/db_xref="cDB:7045354"
/db_xref="taxon:9606"
/clone="2021E8"
/sex="Male"
/coll_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII
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/db_xxef="kaxon:4530"
/clone="nbeb0063017f"
/clone_lib="CUGI Rice BAC Library (ECORI)"
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; Mismatches 0;
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Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                 DB 17;
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Clemson University
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/lab_host="E. coli DH10B"
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/organism="Oryza sativa"
1. .739
/organism="Homo sapiens"
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Seg primer: TAATACGACTCACTATAGGG
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High quality sequence stop: 412.
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100.0%; Pre-
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B79682.1
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library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
                                                                                                                                                                                                                                                                                                                                                                                                               B32178 63.bp DNA linear GSS 17-OCT-1997 HS-1014-B2-E05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 789 Col=10 Row=J, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 63)
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100.0%; Pred. No. 1.2e-08;
tive 0; Mismatches 0; Indels
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Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Scattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 789 row: J column: 10
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0.9%; Score 37; DB 17;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 37; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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B32178.1 GI:2531547
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                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unpublished (1998)
Contact: Mark Adams
Contact: Mark Adams
Lobartument of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
Email: mdadams@tigr.org
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HS-1052-B1-F02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=3 Row=L, DNA sequence.
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Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Zackrone KD, Hood University of Washington Seattle, WA 98195, USA FT: (206) 616-8744 Fax: (206) 685-7301
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M.; Park, H.S., Kim, S. and Kim, Y.S.
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Clones are available from Research Genetics (info@resgen.com). BAC
                                   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seq primer: M13.21
Class: BAC ends.
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/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Korea Research Institute of Bioscience & Biotechnology
52 Ecoun-dong Yuseong-gu, Daejeon 305-333, South Korea
Fat: +82-42-866-4470
Fax: +82-42-8660-4409
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5.2e-08;
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/cell_line="SNU-520"
/lab_host="Top10F'"
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/clone_lib="S21SNU520"
/sex="F"
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Plate: 42 row: B column: 01
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priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayamar Berg method. The coheained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/cell_line="SNU-520"
/lab_host="Top10F'"
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Unpublished (2002)
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Plate: 41 row: A column: 10
High quality sequence stop: 206.
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Best Local Similarity 100.
Matches 37; Conservative
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HS-1017-A2-B08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 792 Col=16 Row=C, DNA sequence.
                                                                                                                                                                                                                                                                                   DNA linear GSS 26-JUL-1999 survey sequence T7 end of BAC
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Gridue du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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The cDNA libraries constructed by this method are full-length enriched cDNA library." 56 c 65 g 46 t
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AT000691 AT8000691 Brassica rapa guard cell Brassica rapa subsp. pekinensis
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Evaluation of 515 expressed sequence tags obtained from guard cells
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  ranalras,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tragged Connectors
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Brassica rapa subsp. pekinensis
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
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/ 29 9 87 t
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                                                                                                                                                                               Contact: Mahairas GG, Zackrone KD, Hood University of Washington Seattle, WA 98195, USA Fax: (206) 665-7301 Email: kzackron@u.washington.edu
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/db_xref="taxon:9606"
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1 (bases 1 to 210)
Mahairas, G.G., Zackrone, K.D.,
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Homo sapiens

Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 221)

3 Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,

Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,

Simon,M. and Venter,J.G.

Building (1998)

10 For a random BAC End Sequence Database for Sequence-Ready Map

Building (1998)

10 Cher GSS: CIT-HSP-2291D16.TR

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: M13-21;
                                                                                                                                                                                                                                                                        AQ006733 27-JUN-1998
CIT-HSP-2291D16.TF CIT-HSP Homo sapiens genomic clone 2291D16, DNA
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HindIII"
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Gaps

Search completed: May 19, 2003, 09:35:37 Job time : 5405 secs

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rhodobact Agrobacte Agrobacte Rhodobact Escherich Escherich

AP003005 MALS91790 SAF010496 MAE009374 MAE008240 MAE018073 MAE018073 MAE005663 MAE

SME591790 AF010496

.1 332635 .5 323450 .4 189370 .3 11164 .3 14945

292.4 268.4 262.2 259.2 259.2

AP003005

D13329 Escherichia AE000503 Escherich

U14003 Escherichia

Xanthomon

AE012535 AAX120210 S

AX065209

Sequence Sequence

Rhizobium

AP002569 E AL603647 F

AF018073 AE005663 AP002569 RME603647

9810 10955 168764

247.4 236.8 236.8 236.2

189333

D13329 AE000503 AE012535

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4 338534 11047

113 114 116 117 118 120 22 23

Mesorhizo

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E50685 Ge AE004660

AB028937 Gluconoba

AB028937 AB063188 AX012443

DB

Length

Match Query

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Run ĕ

E50685 AE004660 AF007800

1458 10977 10031

Sequence Xanthomon

AX120085 AX120085 AE012076 AL627270 AE008765 AE008844

AE012076

5.2 5.2 340000 5.2 349980 5.1 10788 5.1 266050 5.0 2158 4.9 25034

213.6 213.6 213.6 210.2 210 210 206.8 208.8

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14681 199050

202.8 198.4 186.8

Corynebac

Salmonell Salmonell Salmonell Caulobact

Salmonell

Yersinia Yersinia Escherich Escherich

Escherich

AE000251

Mesorhizo

Salmonell

AE005823 AE012823 AJ414147 AE008841 AP002998 N AE005350 E

D90797 E.coli geno D90798 E.coli geno

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AE005449

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286485 11783 11258 14045

181.

D90849 E.coli geno AC084324 Mus muscu Z71688 S.cerevisia

U000007 47 to 48 ce AP002560 Escherich

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                                                                                            (without alignments)
11564.122 Million cell updates/sec
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                                                                           May 18, 2003, 18:00:11; Search time 10356 Seconds
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5.1.6
Compugen Ltd.
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 GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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Gluconobacter oxydans (strain:G624) DNA. Gluconobacter oxydans Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae; Gluconobacter.

1 (sites)
Shibata,T., Ichikawa,C., Matsuura,M., Takata,Y., Noguchi,Y.,
Shibata,T., and Yamashita,M. VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS is the number of results predicted by chance to have a

Pred. No.

AB028937 4073 bp DNA linear BCT 11-JUL-2000 Gluconobacter oxydans gene for sorbitol dehydrogenase, complete

AB028937 AB028937.1 GI:9049448 sorbitol dehydrogenase.

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                             J. Biosci. Bioeng. 89, 463-468 (2000)
2 (bases 1 to 4073)
Shibata,T. and Saito.Y.
Direct Submission
Submitted (15-JUN-1999) Takashi Shibata, Fujisawa Pharmaceutic
Co., Ltd., Fermentation Development Laboratories; Shinkawa-cho
Nakagawara 155, Nishikasugai-gun, Aichi 452-0915, Japan
Fax:81-52-400-1380)
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/strain="G624"
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2737 AACAGCATGCCGACTTCCTTGGTGTATCGGGGGGGAACTGGAAGCAGGTCTTGAAAGCG 2796 [CCCGTTGAGGGCTTGAGGGACCGTTGGCGGGGGGGGGGG	######################################	1 7 1	37 01 97 61	3457 GTTCTGTCCATCCTGCTTCTGGGTCTGGGATGCTGCGGGGGGGTGGTGTTGCTT 3516	3577 CAACATCCGGATTGGCTGGGCCGAAAAGCGGCAGAAGCTAACCGTTCGTCTGG 3636 .	GGTGGTCGCGCGCGTCGAGAAGCCACCAGAGAGGCAAAGCTCTGCTGCGGGACTGCG
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SCGATGGCTGTTCCAAGGTTCTGGACGGAAACCGTGCGT 	SCCAAGGGGACGACTTCGAAAGCTCTTGAAGCTTCTGGGGGGTT CTGGAAGGCGCACTTCGAAAGCTCTTGGAAGCTCCGGGGGAA CTGGAACGGAAC	2017 TGAAACAGAAAACCGCGCTCTGGAAGGACGCGGTTTTTTTT	2137 TCGAACTGTACGGCCATGACGGCACCGAGTTACAAGAAGGATCACTCC 2196 [2257 CGTAGGGGCGCGAAAGATCAAAGCTGTCGGTCGCGCTTAATCCGGTCCCAAGCCGCATTG 2316 [3GGCAGGGGATTTCTG 	497 CGATTGTTGCCGCTTTCGGCCCGGTCCCCTGCCCGCGCGCG	GCTGCAGAAATCGATTCCTTCGGTGAAGCTCGGGGTGGGGCCGGCTG 3CGATACGGAACAGTGCCGTCATCAGGTTCTCAAGCGCGCCGTATTATCGG 11111111111111111111111111111111111

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PSTIFGYVVEGLRRRRDAGGKAFTIMSCDNLRHNGNVARKAFLGYAKARDPELAKWIE
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for L-sorbose reductase, complete
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/note="synonym of NADP-D-sorbitol dehydrogenase"
(NADP-SLDH), homolog of NADP-SLDH with the accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Gluconobacter suboxydans subsp. suboxydans)"
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NADFH-dependent L-sorbose reductase is responsible for L-sorbose assimilation in luconobacter suboxydans IFO 3291
J. Bacteriol. 184 (3), 861-863 (2002)
21650687
   AAGCCCATTGTGCGGTTTCGGAAACATCAGGGTCCGGATCACTCAGCAGCTCCCGCGCAG
                                                                 CGGTTGCGTCCAATCCGTTTGACCGGAGAGCCCAGAAAAAAACGTCCGGAATGTCGCATTA
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                                                                                                                                                                                                                                                          Submitted (13-JUN-2001) Masako Shinjoh, Nippon Roche F
Center, Applied Microbiology; Kajiwara 200, Kamakura,
247-8530, Japan (E-mail:masako.shinjoh@roche.com,
Tel:81-467-47-2226, Fax:81-467-45-6812)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gluconobacter oxydans (strain: IFO3291) DNA,
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/note="originally submitted as '
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Shinjoh,M.
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	TCCTGAACAAAGACGTCATCCCG ATCGGGACAGCGTCATCAGCCGT ATCGGGACAGCGTCATCAGCCGT	1617 TTCTCCAACAGGGGATGTCGGACCACGGGTTGCGGACGGGTGTTCCAAG 167 1617 TTCTCCAACAAGGGATGTCGGACCACGACGGCTCCGGATGCTAGCGATGGCTGTTCCAAG 167 1011 11 1 1 1 1 1 1 1 1	1677 GTTCAGGTGTTCTGGACGGAAACCGTGCGGCGATCGAAGACAAGCGGGACCTGTCA 1	AGGGC 1	AGGCG 1	13	TAAAA 19 CAAG 14		SULT 3	DNA linear PAT 06-SEP-2000 DEFINITION Sequence 1 from Patent EP0955358. ACCESSION AX012443 ACCESSION AX012443 1 CT.0000482	S Gluconobacter oxydans. ISM Gluconobacter oxydans. ISM Gluconobacter oxydans	REFERENCE 1 (bases 1 to 1458) THTTE Contion to continuous 1 to 1458 1 to 145	AL PATENT: EP 095338-A 1 10-NOV-1999; HOFFMANN LA ROCHE (CH) S Location/Qualifiers	329 a	Watch 23.2%; Score 955.6; DB 6; Length 1458; Local Similarity 78.5%; Pred. No. 6e-183; hes 1144. Conservative of Mismatches 314. Indels of Cap	537 ATGATTACGCGCGAAACCCTTAAGTCTCTTCCTGCCAATGTCCAGGCTCCCCCCTATGAC 59 1111 1111 1111 1111 1111 111 111 111	597 ATCGACGCATCAAGCCTGCCATTTCGCTGTAGGTAACTTTTTCGAGCCCAT 6

	957 ACCGGTGCGTTCGATCTGGAGAATGCGGCAGTAAAGGCCGACCTCAAGAACCCGGAAAAG 1016 1 1 1 1 1 1 1 1 1 1	AAGGCTTTACGGTCATCTCTGTGATAACCTGCTCATCACGCGAATGTCGCCCGCAAGAAATCGCCCGCAAGACGCTATACGGCAATGTCGCCCGCAAGACGCTATACCGCCATAACCGCATAATCTCGCCGCATAATCTCGCGGATAATCTGCGGATAATCTGCGGAATGGTCGCCGCAAGGCCTTCGTCGCGAAGGCCCGCAAGACGTTGGCGAAGGCCCGAACGGCCCAAGGCCCGAAGGCCCGAAGGCCCGAAGGCCCGAAGGCCCGAAGGCCCGAAGGCCCGAACGGCCCAAGGCCCGAAGGCCCGAACGCCCAAGGCCCGAACGCCCAACGCCCAAGGCCCCGAACGCCCCAACGCCCAACGCCCAACGCCCAACGCCCAACGCCCAACGCCCAACCGCAAATCGCCCCCCAACCCCCAACCCCCAACCCCCAACCCCCAACCCC		1437 GGCCATGCTCGTGCTTCCCAGGCATTCTGGTCGGCTATGAGAATGTGGATGACGCC 1496 11	1557 ACCCTGAAGGCGCCTTCAGGCATGACGCTCGAAGGCTATCGGGACAGCGTCATCAGCCGT 1616 1021 ACCCTGAAGGCACGCGGGATGACGCTGGAAGGCTATCGGGACAGCGTGATCAGCGCT 1080 1617 TTCTCCAACAAGACGATGTCGGACCAGACGCTCCGGATTGCTAGCGATGCTTCCAAG 1676 1617 TTCTCCAACAAGACGATGCCAGACGCTCCGGATTGCTAGCGATGCTTCCAAG 1676 1111	1677 GTTCAGGTGTTCTGGACGAAACCGTGGGGGGACCTGTCA 1736 1141 ATCCAGGTGTTCTGGAAACCGTGCGCGCATCGAAGCGGGACCTGTCA 1736 1141 ATCCAGGTCTTCTGGAAAACGGTCCGCAAGGCTTTTGAGGCCAAGCGCGTCTGTCC 1200 1737 CGTATAGCTTCGGAATTGCATCCTATCTCGAAATGCTGCGGTGGTCGCGACGAGAGGC 1796 1101
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CDS	gene CDS	dene .	aeue	CDS	gene
1261 GGCACCTACGAGCCATTCGAGCCGACTTTTGGTGACAACCATAAGACTCTGGCCAAGGCT 1320 1857 GACGACTTCGAAGCTCCCGGCGTTCGATGGTGGCGCGATCTGGATACG 1916 11	AE004660 N Pseudomonas aeruginosa PA01, section 221 of 529 of the complete genome. AE004660 AE004091 AE004660.1 GI:9948372 Pseudomonas aeruginosa. Pseudomonas aeruginosa. Pseudomonas aeruginosa. Pseudomonas aeruginosa.		Stover, C.K., Pham. XO.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.KS., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E. W., Lory, S. and Olson, M.V. Direct Submission Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington, Box 332145, Seattle, WA 98195, USA	e C	// 1012 /gene="mtlR" /godon_start=1 /codon_start=1 /codon_start=1 /transl_table=11 /product="transcriptional regulator MtlR" /protein_id="AAG05725.1" /protein_id="AAG05725.1" /do_xref="GI:9948373" /translation="MPRASKYDPSYELMDDHEGHSLIYR0HGFPSPLVRWHFHKEYE LHIAVASSGKVFIGDYIGNEAPPLICHTGPRIPHWISQVEPDEVVARRDMINVFTDE VLEDGSGVFSELNRLAPLLARARYGIEFRDPALIGESRRLLQRIADSGGMTRLGYFFI LMMQLAECEDYOLLSTVFSSGLADEHNVERINRANDYIFOHYAQDLTGEGNARLGYF PTYFSRFFRQAGRGFVEFVNRLRISKSCELLARSELPVTEVCFESGFSNLSNFNRRF QQLKGMTPPGSYRRLYTQRLTEQNLL" /gene="PA2338"
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Best Local Similarity 55.5%;
Matches 726; Conservative
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LLYPGENQFVGLENFTYFITDSGFLPGATNTLLLVGSVLLISVVFGVLISALLEASEF
LGRGIYRVLLLISPFFMPTVOGALINNALIFHPYGSILANVKFRGAEPVDULAHTPLL
SITTIVSWOWLPFATLLLMYRANGSLDOEDKEAARLDGAGAIA.FWHTPLPHLARPIAV
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KTKSTLLMMLSTKMLPPVGVLMPITLAKSRGCLDTRÄLLIITTLINLDIVVWNYY
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TSSNAAPLTALIASYSSPEGLFWAKLSAVSTLACAPILIFGWISOKOLVRGLSFGANK
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LSNLDAALRVQMRLELARLHKELQATMIYVTHDQVEAMTLADKVVVLNSGRIEQVGSP
LELYHQPANLFVAGFLGTPKMGFLKGKVTRVDGQGCEVQLDAGTLISLPLSGASLSVG
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QYGETLHLHIDPAHCHLFDTDGVAVAVPLRAAA"
5258. .6739
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SDMLLAEDSAQALIDKLASPEIRIVSLTITEGGYCIDDSNGEFWAHLPQIQHDLAHPS
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KAHVSFPNAMVDRITPMTSTAHRLQLHDEHGIDDAWPVVCEPFVQWVLEDKFVNGRPA
WEKVGVQFTDDVTPYEEMKIGLLNGSHLALTYLGFLKGYRFVHETMNDPLFVAYMRAY
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                                                                                                             /note="similar to E. coli MalF protein; inner membrane
                                                                                                                                 subunit of the periplasmic binding protein dependent mannitol transport system"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to E. coli MalG protein; inner membrar subunit of the periplasmic binding protein dependent mannitol transport system"
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/gene="mtlF"
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Pseudomonas fluorescens mannitol operon, MtlE (mtlE), MtlF (mtlF), MtlG (mtlG), MtlK (mtlK), mannitol dehydrogenase (mtlD), xylulose kinase (mtlY) and fructokinase (mtlZ) genes, complete cds.
                                                                                                                                    SQIGEFAAKLTDKSKEQYGLCLRGKAGWGENMALITTLANGYGARWFDEKWQPEFNGP
EWKDALNFYVDNMKKSGPPGASSNGFNENLALFNSGKCAIWVDASVAGSFVTDKTQSK
1698 ACCGTGCGTCGGCGATCGAAGACAAGCGGGACCTGTCACGTATAGCGTTCGGAATTGCA 1757
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/translation="MKFTAKALLACTCMTLSAVSLGAQTLTIATVNNSDMIRMQKLSK
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DGVANVPPGTRKSTYSDEYMKAAPFAKVTLESLKVADPTKPTLKPVPYIGIQLVTIPE
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Structure and function of the genes involved in mannitol, arabitol
and glucitol utilization from Pseudomonas fluorescens DSM50106
Gene 206 (1), 117-126 (1998)
98121321
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Bruenker, P., Altenbuchner, J. and Mattes, R.
Direct Submission
Submitsed (10-JUN-1997) Institute of Industrial Genetics,
University of Stuttgart, Allmandring 31, Stuttgart 70559,
On Aug 4, 1997 this sequence version replaced gi:2065484.
Location/Qualifiers
                                 /note="similar to E. coli periplasmic maltose binding protein MalE; periplasmic subunit of the periplasmic binding protein dependent mannitol transport system"
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Brunker, P., Altenbuchner, J., Kulbe, K.D. and Mattes, R.
Cloning, nucleotide sequence and expression of a mannitol
                                                                                                                                                                                                                CCGACTTATGGCGACGCCGAATGGAAGTTGGCCAAGGCGGACGACTTCG 1866
                                                                                                                                                                                                                                                 FQAIGTQVGKFFSGALTGQQTVDAALTAAQTTTEREMKRAGYPK"
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/db_xref="taxon:294"
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/product="MtlE"
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932. .2242
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Mesorhizobium loti
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                           ACGGAATGGTTGATCGCATCACCCCGACCGTTTCGGCGGGAAATCGCCAAGAAGCTCAACG
                                                                                                                                                                                                                                                                                                                                 ATGAACACGGCATCGACGATGCTTGCGAACCCTTTGTGCAGTGGCTAC
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   5634 TCGTCTCGCTGACCATCACCGAAGGCGGCTACTGCATCGACGACAGCAACGGCGAATTCA
                                   ATCTGGAGAATGCGGCAGTAAAGGCCGACCTCAAGAACCCGGAAAAGCCGTCTACCGTTT
                                                          TGGCCCACTTGCCGCAGATCCAGCACGACCTGGCTCATCGTCGTCGCCAAAAACCGTGT
                                                                                                       TCGGTTACGTGGTCGAGGCCCTGCGTCGTTGGGATGCCGGTGGTAAGGCATTTACGG
                                                                                                                                                                           TCATGTCCTGTGATAACCTGCGTCATAACGGCAATGTCGCCCGCAAGGCCTTCCTCGGCT
                                                                                                                                                                                                           TGATGTCCTGCGATAACCTGCCCCACAATGGCGCTGTCACGCGCAAGGCACTGCTGGCGGT
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AP003005 BA000012
AP003005.2 GI:14024756
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FADOPNVSPOASVATFCSSGGGMLEDLICTMMLIVATGVIRELFELDINAFNALVEDÂP
IGABGVSMLPFLNGERVPALPHATGSLHGLTWTNLTRANLCRAVVEGTTFGLRYGLDL
LRHTGLQSOSIRLIGGGSKGSPVWRONYADINNTEYICTBOSGRAALGAAIQAAWSOSG
ESLASLCDKCVSVDPASRTLPVAANVGAYQLAYEŖYQOHVATL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MYLVCGBALFDEFSEEDASGQASKVTYKAIAGGSPFNVAVGLRR
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WYLNRPQPDIQLWNDRVAELAKHADLIKVSDEDLHLLYPGGSFESVLGGWLGHRCOLV
FLIRGGDGASVFSRQHGTWSQPAQRVWADTVGAGDTFQAALIAWLTEHQLDSVQGLQ
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LIADGRETERAALVVAAWALYLKGVDENGVSYTIPDPRAEFCQGLVSDDALISGRLLA
VEEIFGTAIPNSPEFVAAFERCYGSLRDNGVTTTLKHLLKKPV"
VGEOS. .8410
/geoe="mtly"
6229. .8410
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LLPHDYLNYWLTGRAVAEYGDASGTGYFNVRTRAWDMALLKHIDPSGRLEAALPTLIE
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GRREQHTQEWLDAFTEATHRALQQAGVDGQDILGIGVSGQQHGLVLLDDSGQVLRPAK
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glucose and glucitol"
/note="MtlZ"
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3194 c 2919 q 1877 t
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Pred. No. 6.1e-56;
); Mismatches 590;
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                                                                                                                                                                         /product="xylulose kinase"
/protein_id="AAC04473.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAC04474.1"
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/transl_table=11
/product="fructokinase"
                                                                                                                                                                                                         /db_xref="GI:2293419"
                                                                                                                                                           /transl_table=11
                                                                                                                                         /codon_start=1
                                                                                     /qene="mtlY"
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SQVLYYLAENLSGRAGEFAARLTELTGATPKAAREEVDQSIERLFLYAGLADKFEGRV
HQPPARAVTLALHEPVGVVGIVAPDASPLLGLISLVAPALAMGNTVVAVPSERYPLLA
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HGLAPLSTRLQEIEASVRDGADEIDVVIPRGLVFGAKWRELYNEIVSMRAACGDAHLK
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TGYLIGFKPAGGISTAKASLDWLVLMKEELGRPWLEPELFRFGASSLLTDIERQLEHH
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NASVQPILERYVERLRKELAAKGYARDFLIMNGNGGMISARFVTRESAKTVMSGPASG
VIAAAYTGKRAGFENLVTYDMGGTSTDVALIRNAEPAVSNEIEIEYAMPIHVPMVAVH
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VAVLDETQLHHVLERHRNBGEQLIGKEAVKPETIRVTHSADMQFVGQTHIINVPLPSS
TVTRQELQALFEKAYFARFKVELPEIRANLVNLNTSVTGVRPAIDLSRLIDPAGRAKT
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GTHLMDVRFAMPVYRAGKIFCWLSNTGHWPDIGGSVPGGFSASATAVEQEGLRLPPVK
LFKKGVLDPEIYAIICSNIRVADQRIGDIRAQAAALLIGQDRLNGILDRYGDETVVEA
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GSSKPCAGPMNSVLATTLSSVYLAMRHIFPDVPISAGAFEPLIVRRPEGTFLDAKYPR
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QVGDTVIMRQKSTGTLVVDALTPAKRLFMISTGTGIAPPASLLRDPDTYEKFDQLILT
HTCRDNAELTYGQELVAALESDPLIGELTTGRVTLYNSTTREESARMGRITALIGSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB51364.1"
/db_xref="G1:14024762"
/translation="MKENFSVQPPDSLGSVAAGIDVGGTFTDLLLIDGRDGGKVHIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPTTVDNQAFGVVSALGATGFAIDGIDLIVHGTTTTNAVLERRLARTGMITTRGFRD
VIELGRRTRPQPYGMTGTFVPVIPRNLRLEVSERVEASGAVRTPLDEAEMREAVTALI
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LAVDNPVTVERVYGIFADKIGKATGLSGVEAAGAVLRLGNMKMAGAIRMVSVSRGHDP
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   LFIGGKQVRPDGNYSLAVATAKGKLAGEVGFGNRKDIRDAVSAARACKGWPEATAYNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MNTTSAFNTAGARPLQFPIPANVYAETVVSVKHYTDRLFSFRIT
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                                                                                                                           NLKRVWSGNGRSLDWASDEAAGDAFLRRAVEVKNVWVPYGD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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/db_xref="GI:14024763"
                                                                                                                                                           complement(4478. .5524)
                                                                                                                                                                                                                      complement(4478. .5524)
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/gene="m114785"
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/transl_table=11
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6753. .8837
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/gene="mlr4786"
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8854. .10596
                                                                                                                                                                                     /gene="ml14784"
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SAIVGPDDDVLIPRGSEKTDWEVELAVVIGKTAKYVSEADALDYVAGYAVAHDVSERA
FQAERQGQWTKGKSCDTFGPTGPWLVTKDEVADPQNLKMWLTVNGKTMQNGSTKTWVY
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ELAKFPGIKTEKLDVLNDEAVNTTFAETGRVDVLFNCAGFAHGSSILLEMBKDGDDFAF
NLWYRAMIRTIRAULPGMLERGDGSIVNMSSYAGAGKGYPNRRAYGYTKAAVIGLTKA
IAADYVGKGIRCNAICPGTVESPSLQDRWHAQGDYEAARAFIARQPMGRLGTPEEIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MKLLRYGEVGSERPGLLDADGTIRDLSAHVADIAGTTLHPASLE
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FAVLESIDNGKPIRESRDIDVPLAIRHFIHHAGWAQALDRDFPGHKGVGVVGQIIPWN
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GAAIVNHPGIQKIAFTGSSEVGKIIRKATAGSGKKLSLELGGKSAFIVFEDADLDSAV
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DLTQLDRVKGLVAEGAKQGAVCWQPDAALPSSGYYHLPTLATGVSPANILAQEEVFGP
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ACGFGGYRESGFGREGGREGMFEYLTAKLPLGPVIKPAAVSAQPVEQADGAAIDRTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVKYLVSYLSQFMSLHPGDIISTGTPPGVGLGMKPPVFLRAGDVVELGIEGLGQQKQT
                                                   Kaneko,T., Nakamura,Y., Sato,S., Asamizu,E., Kato,T., Sasamoto,S., Watanabe,A., Idesawa,K., Ishikawa,A., Kawashima,K., Kimura,T., Kishida,Y., Kiyokawa,C., Kohara,M., Matsumoto,M., Matsuno,A., Mochizuki,Y., Nakayama,S., Nakazaki,N., Shimpo,S., Sugimoto,M., Takeuchi,C., Yamada,M. and Tabata,S.

Complete genome structure of the nitrogen-fixing symbiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="2-hydroxyhepta-2,4-diene-1,7-dioate isomerase"
/protein_id="BAB51359.1"
                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-DEC-2000) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research: Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail: kaneko@kazusa.or.jp, URL.http://www.kazusa.or.jp, Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3935(ex.2338), Pax:81-438-52-3935(ex.2338), Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="aldehyde dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .332635
/organism="Mesorhizobium loti"
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Phyllobacteriaceae; Mesorhizobium.
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/gene="ml14781"
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/gene="ml14783"
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/db_xref="GI:14024757"
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DNA Res. 7 (6), 331-338 (2000)
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/gene="ml14780"
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/transl_table=11
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Direct Submission
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                                                                                      CGTTTCGCTGACCATCACCGAAGGCGGCTATTTCATCGACCCGGCGTCGGGCAAGTTCAA 107566
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Capela, D., Barloy, Hubler, F., Gouzy, J., Bothe, G., Ampe, F., Batut, J., Boistand, P., Becker, A., Boutry, M., Cadieu, E., Dreano, S., Gloux, S., Godrie, T., Goffeau, A., Kahn, D., Kiss, E., Lelaure, V., Masuy, D., Poolt, T., Poorteelle, D., Punchler, A., Puncalle, B., Ramsperger, U., Renard, C., Thebault, P., Vandenbol, M., Weidner, S. and Galibert, F. Analysis of the chromosome sequence of the legume symbiont
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                                                                                                                                                                                                                                                      107565 CCCAGCCCATCCGGGATATCGTCGCCGACGCCCAACCGGGCGCCCCAAAGACAGTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1571 TTCAGGCATGACGCTCGAAGGCTATCGGGACAGCGTCATCAGCCGTTTCTCCCAACAAGGC
                                                                                                                                                                                                                                                                                                                                                           107445 GATGTCCTGCGACAACATTCCCCACAACGCCCATGTCACCTCGGATGGCGTCATTGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                       1151 TGCGAAGGCGCGCGCTCCGGAGTTGGCGAAGTGGATTGAGGAAAACGCGACCTTCCCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGCGCGCTGATCGATGAGGATTTGGCCGGTTGGGTGAGCAGCAACGTCGCCTTTCCAAA
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                                                                                                                                   TCTGGAGAATGCGGCAGTAAAGGCCGGACCTCAAGAACCCGGGAAAAGCCGTCTACCGTTTTT
                                                                                                                                                                                                                          CGGTTACGTGGTCGAGGCCCTGCGTCGTCGTTGGGATGCCGGTGGTAAGGCATTTACGGT
                                            CGTTTCCATGACGATCACGGAAGGCGGCTACAACATCAACGAGGACGACCGGTGCGTTCGA
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                      /translation-"MRLFGRFVLAASVALTLASGAASAQDKLRIGTEGAYPPFNYANA
DGTLGGEDIDLGKALCAEMKAECEFTVQDEDGSIPALQAGKEDAINITITPERAEKY
EFTHKYYQTPPAITVPKASTAGTSPDDLKGKALGVQTATIHQKFAEQKYSGSTVKAY
PTGDDARTDWANGRIATAMMOSSILITFWLKKPDGACCKLLGTLTADPAIHGPGVGIAL
OKGNKELAGKFNAAIDALRANGKYKEINDKYFSFDVYGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLEKAMISDADLDGLKRWAFTSGHVNGTRVLISRTGVTGELGFELFVPADEAASVWDTL
MRAGKDFGLKPYGVLAMFTLGLEKAYPAHGIDMDETRTPFHVGLDRWIKFDKGDFIGR
EALLKIRDKGLDERWTGLILDGNKPAATDARVLADGEDAGIVTYSDHGYSLGKVLATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="ABC transporter, permease protein"
/protein_id="BAB51388.1"
/db_xref="Gi-19424766"
/translation="MSPILFELLLRSIWETVLMTAASGLISLVFGLPLCLALISTERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTRANVGVQDLSTWGKMDIKGPDAEALVNHVIVNDAVAMKPGQVRYSTVCREDGGIMD
DLTVFRLGPEHFMLVTGSVNRLKMLPWLQHHAQGRKAYVTDITAAVAFPTIQGPRSRE
                                          FGLAYEVEILRGDARASFVMDHGRFGPQGALGGKDGEPNSVTVFRGGVAHVPPHLSKE
QDIPLKAGDRVRVGTPGGGGYGDPRERDADQVQRDVALGYYTAEEASEKFGVVLSADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="METFLAERRSPFYSSIVGLGATMGRVGGDF1SAKYYSGVTDEHL
PVSGCAAEVSQRIAEAVFAAMVQALPDKVTAAPAGSSGNFALGGNDPARGRDYVMYQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610
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                                                                                                                                                                                                                                                 'product="amino acid ABC transporter, periplasmic amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        551 AACCCTTAAGTCTCTTCCTGCCAATGTCCAGGCTCCCCCTATGACATCGACGGGATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTGGGATCGTGCATTTCGGTGTAGGTAACTTTTTTCGAGCCCATGAGGCGTTCTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAGCAGATTCTTGAACACGCTCCGGACTGGGCGATTGTTGGTGGTGTTGGCCTGACGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107859 CGACGATCTGTTCAATTCAGGTGTCGGCCATGACTGGGCGCTGGTCGGCCGCGCGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGACCGTTCAAAGAAAAAAGCCGAGGAATTCAAGGCCCAGGACTGCCTGTATTCCCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAGGGCGAGAAGATCGGTCGCGGCAAGCTCGAAGAGCAGGACTGGCTGACCACGGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGAGCAGGAT --- GAAGGCCATATGAGCGCCCGTGTCACCGGCGCGATGATCGATTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="aminomethyltransferase"
/protein_id="BAB51367.1"
/db_xref="G1:14024765"
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                                                                                                                                                                                                                                                                    acid-binding protein"
/protein_id="BAB51366.1"
/db_xref="GI:14024764"
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10720, 11/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="mlr4790"
11674. .12801
/gene="mlr4790"
/codon_start=1
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/transl_table=11
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/transl_table=11
                                                                                                                                                        10720. .11493
/gene="mlr4789"
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                                                                                      LTVDRKATDGQRAG"
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Best Local S
Matches 616
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JOURNAL

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Plantes-Microorganismes, UMR215-CNRS-INRA, BP27, F-31326 Castanet,
France, Laboratoire de Genetique et Developpement UMR6061-CNRS,
Fraculte de Medecine, 2 avenue du Pr. Leon Bernard, F-35043 Rennes,
France, GATC GmbH, Fritz-Arnold-str. 23, D-78467 Konstanz, Germany,
Universitaet Bielefeld, Biologie IV (Genetik) Universitaetstr 25,
D-33615 Bielefeld, Germany, Unite de Biochimie physiologique,
Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20,
B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Faculte
des Sciences Agronomiques de Gembloux, Avenue Marechal Juin 6,
B-5030 Gembloux, Belgium. E-mail:Jerome.Gouzy@toulouse.inra.fr
Location/Qualifiers
                                                                                                                                            Gouzy,J.
Direct Submission
Submitted (26-JUL-2001) Gouzy J., Submitted on behalf of the MELILO
EU Consortium
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PEPRDRGYGYSEPGEFTGAIPEYRDIAPAPVEREDLPNSLPSLSDREEAAYDPQYDDP
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EMLGEKFHMDEAYLRELNPGVDFSIPGTTIKVVNPGPNKKGKVARIVADKARKQVLAY
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GPNGPVGTVWIALSKPTYGIHGTPEPSKIGKTQSHGCVRLTNWDATELGKMVSTGVTV
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GDGPSFVYDLVAKHGIBCEAVRNGTLHMSVGABGLKEIREREAQWKKRGAPVEVLSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:092K34"
/translation="MTPATRTGLSLFAALALMAMELAPANAQDAYGGYWGGGDVMLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAQPMPPAMTVTGKSRAEIAALQVFLDREGFSPGVIDGKMGSNVTKAIEAWOOATGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="miscellaneous; hypothetical/partial homology"
Sinorhizobium meliloti strain 1021
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001)
21396507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="PUTATIVE OXIDOREDUCTASE PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Product confidence : hypothetical
Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="small molecule metabolism"
/note="Product confidence : putative
Gene_name_confidence : hypothetical :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sinorhizobium meliloti"
/strain="1021"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
/product="HYPOTHETICAL PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAC46788.1"
/db_xref="GI:15075232"
/db_xref="SPTREMBL:092NJ3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
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/db_xref="GI:15075231"
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predicted by Homology
predicted by FrameD"
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predicted by FrameD"
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/gene="SMC01576"
1707. .2006
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/gene="SMc01576"
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                                                                                                                   REFERENCE.
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FEATURES

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WNLKTPRGTVTARHVILATNAYGSLVTGVPWKEYRQELTILPYFQFATNPLPDNVAAR
ILPERQGAWDTGLVWTSFRAMRQNNLLFGSIGRLDAIAAGTHRAFAARSVRKLFPYIG
DEREHWWDGRIGWTTNNLPAMHVIAPNVSTSGYNGRGIAPGTVFGRALARHVTGDT
SAIPLAETPVTPDPWRTLKSAFYHAGAQAKHFIDKRF
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SASHVKKVIFHPKFLPGVTICDPELTVGMPKVITAGTGMDAFAHCLEAYSSPFYHPMS
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IYNTHHGWTNAVVMPPVLRFNRSAIERKIGRAAYLGIAGGFDGFYDVVLRLREELGV
PDKLSALGVGTDRIDEMAEMAIVDPTAGGNPVEITLDAAEKLFAECI"
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                                                                                                                                                                                                                                                                                                                complement(3024. .3740)
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/function="miscellaneous; hypothetical/global homology"
/notes="Product confidence : hypothetical
Gene name confidence : hypothetical
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/gene="SMc01582"
/EC_number="1.1.1."
/function="Small molecule metabolism"
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Gene name confidence : hypothetical
predicted by Codon_usage
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/db_xref="GI:15075233"
/db_xref="SPTREMBL:092NJ2"
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/transl_table=11
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complement(3949. .5094)
/gene="SMc01582"
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/gene="SMc01579"
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complement(5091. .6476)
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Direct Submission
Submitted (26-JUW-1997) Institute of Molecular Genetics, Flemingovo
2, Prague 16637, Czech Republic
Location/Qualifiers
1. .189370
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                                      AGCCGTCTACCGTTTTCGGTTACGTGGTCGAGGCCCTGCGTCGTCGTTGGGATGCCGGTG
                                                                                                                   GTAAGGCATTTACGGTCAFGTCCTGTGATAACCTGCGTCATAACGGCAATGTCGCCCGCA
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Proc. Natl. Acad. Sci. U.S.A. 94 (17), 9384-9388 (1997)
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strain SB1003, partial genome.
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                    AAGTETGLGLELGGRDPGYVMEDADLDAAVDTLMDGATYNSGQCCCGTERIYVHESLY
BYEVEKSVAWSNYKLGNPLDPETTLGPMANKFRAATVRNQVADAISKGARALIDPKL
FPQDDGGAYLAPQVLVDVDHGMEFREETFGPAVGIMKVKSDAEAIELMNDSRYGLTA
SLWTKDAERAARIGRDLETGTVFMNRADYLDPALCWTGVKETGRGGSLGYLGFHNLTR
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DKNGOYGMSELMRHYVAGQLAHASEVTYFLAPYINSYKRFMAGTFAPTKAIWSKDNRT
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KEVREIPHTLREAGEALSGSKMLRAAFGEEVVDHYVHAAEWEQQEYDRRVTDWEVARG
  ILVGERMVRAFIEAGVPADVFQNLFLDHDTTAALIAAKSFDFINFTGSVEGGRSIERA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDMLDHDTHAEVPHSPRAILKKQVARLEAMGFKAYMASELEFFLFDQSYDDARLSGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLQLASGYNEDYHIFQTTKEEDVMRAIRNGLQGAGIPVENSKGEASAGQEEINVRYAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACCGGTGCGTTCGATCTGGAGAATGCGGCAGTAAAGGCCGACCTCAAGAACCCGGAAA 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transport of small molecules;
                                                                                                                                                                                            /function="miscellaneous; hypothetical/global homology"
/note="Product confidence : hypothetical
Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATGATTACGCGCGAAACCCTTAAGTCTCCTGCCAATGTCCAGGCTCCCCCTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATCGACGGGATCAAGCCTGGGATCGTGCATTTCGGTGTAGGTAACTTTTTGGAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246932 GCCGGCATGACCTTCGGGCCGGCATCGTGCACTTCGGCGTCGGCAATTTCCACCGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGAGGCGTTCTACGTCGAGCAGATTCTTGAACACGCTCCGGACTGGGCGATTGTTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGCCTGACGGCCAGTGACCGTTCAAAGAAAAAAGCCGAGGAATTCAAGGCCCAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246812 TCGGCGCGGGTGTCCTGCCATCGGACAAGGTCATGCGCGACAAGCTCGAAGCGCAGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCTGTATTCCCTGACCGAGACGCCTCCGTCCGGCAAGAGCACGGTGCGCGTCATGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCTGCGTGACTATCTGCTTGCCCCGGCCGATCCGGAAGCCGTGCTGAAGCATCTTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATGATCGCCTA---CCTCGAGCCCGGGACACGCCGCGGATCGTGGCGCAGCTCGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCCGGCCATCCGCATCGTTTCCATGACGATCACGGAAGGCGGCTACAACATCAACGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 323450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                          'product="CONSERVED HYPOTHETICAL PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 268.4; DB 1;
Pred. No. 3.6e-44;
0; Mismatches 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="cell processes; tranamino acids, amines, peptides"
                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="SPTREMBL:092NI9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by Codon_usage
by Homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(8131. .9678)
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                                                                                                                 complement(6674. .8038)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(8131, .9678)
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                                                                                                                                                                                                                                                                                               FrameD"
                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                             predicted by
                                                                                                 PKSYHLKKVTA"
                                                                                                                                                                                                                                                      predicted Predicted P
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607; Conserv
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Best Local Si
Matches 607;
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CDS

CDS

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GLDVAAQA I YRDSVAAGESRAQDK I VA IEPTGPLAPLRADLARLAGLARDLARPGSRD
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                                                                                                                                                                                                           ARTIERRARDLVASALRLARSLESYDRESAALEAARAVVAGOMQUEPDLRPLIKT
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PGLEVVMIGHSEIVGKPVAFLLMAEGATVTVCHHWTRSVAMHSRRADVVIVAVGKAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSSEQISRITSVIDDIAFQTNLLALNAGVEAARAGEAGRGFAVVASEVRGLAQRSSEA
AREIAGLIAŢSVRQVGEGVELASGSDAALGRIEDLVSRLDALLAAIETGAGEQSAGIS
                                                                                                                                                                                                                                                                                                                                                                                            RIETAFPAAYEGLRSDFNQAVTRMAELLSEIVRASGSVOSEAHQLGAASGELGRRTET
QAASLEETAAAMNQMAASVAQALQGAREAARAVGQTRETTAAGREVVRRTLQAMTDIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LACASFGRLLGVDWLAFGPVWLAGAIGQYIRHHLLHRGVNIFIVAGAIAFLSATLGGL
GAIALQSGTVQLAMMASILLLVPGVPSTNAQTDIMDGYPTMGSARAVWVLMIMLFAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILDAMCLALYGDAPRLSAGARSDKVPDAAGEEISAADSRAILRRGAATGWAEVRFAG
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EEFRRTVLLAQGDFDAFLRADTGERATLLEKVTGTGLYRAVS I RVYERTEMARAEHAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLARAAEHRLLDDAARAALTEEIAARTAATAAATAERAGLSEALARHRRHAEAVRQVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAALAGAEALQAEAGPARAQLDRLERAAPLHLPWQAAAEARARLDAARSGAEAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="potential exonuclease"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGRIRPSFAQDYQDLALVRREGGHS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(12010. .12912)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLMRNALTAHRRQVAAGWLEAAKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (13007.
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="sbcC
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PNPTRSSYLTALQDLRDVDLDGLQFLQFGPGDNQGLDQVFLTEISPAGTIAELTPAATP
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/protein_id="AAC16114.1"
/organism="Rhodobacter capsulatus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product-"hypothetical protein"
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/db_xref="GI:3128259"
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/protein_id="AAC16112.1"
/db_xref="G1:3128260"
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                                                                                                                                                                                                                                                                                 /protein_id="AAC16109.1"
/db_xref="GI:3128257"
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/db_xref="GI:3128258"
                                                                                                                                                                                                                                                   protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(453. .2471)
/EC_number="2.2.1.1"
                                                              'db_xref="taxon:1061"
                                                                                                                                        complement(<1. .456)
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                                                                                                       /chromosome="1"
                                                                                                                                                                                                                                                /product="CobD
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'gene="mcpA"
.897. .9542
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AGGIGCIGCCGATCGIGCCGCCGGTCCCCGGGCAGGATCIGAACGATTACAAGGCGCTGA 128979
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                                                                                                                                                                                                              CGGAAATCGCCAAGAAGCTCAACGCGGCCAGTGGGCTGGATGACGACCTGCCGCTGGTGG 1305
                                                                                                                                                                                                                                                                                                  CCGAGGATTTCCATCAGTGGGTGCTGGAAGACCAGTTTGCGGATGGCCGTCCGCCGTTG 1365
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Agrobacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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Wood,D.W., Setubal,J.C., Kaul,R., Monks,D., Chen,L., Wood,G.E.,
                                                                                                                                                                                                                                                                                                                                                                                                             TGCTCAATGCAGGCCATGTCATGCTCTGCTTCCCAGGCATTCTGGTCGGCTATGAGAATG
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                                                                                                                                                                                                                                      129338 GCGATCGCGAACGGGCGATGGCCGCTGATCTGGCCTTGACGATGCCGCCGGTGACCT
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                                            TCGCCCCCAAGGCCTTCCTCGGCTATGCGAAGGCGCGCGATCCGGAGTTGGCGAAGTGGA
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AE009374 AE008689
AE009374.1 GI:17742928
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GVVVLCGTLSRCPGGMDLDRHITPLRDRAGOIRAOVLALPETROADLPGELEGABEEGTE
GAVTAALLAETLAETRARAAA TAGTLEI IAMAHLTCAGGLESAGAERRILIGGDHAVP
DVFPPALAHVALGHLHRPQSLDGGRVRYSGAPFPLSASEIGYDHGVTLLDLAGGAAPR
HIPLPRPVPMLRLPAGGTAPLPEILAALDRLALDBRABGPPLYLALBADGRAPR
AALDAALEALPLRAGGITTRPETARPAAAPPQDLTRTTPEALFAAAFRDHGTEPET
RHLSAPRALSLELL
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                                                                                                        EAERRAQEIGOLSAELARDAATRAALAGLAVETEAARAELEVWEAVNKAIGARSGDRF
ARIAQAITLDVLVERANRHLADLNPRYRLRRAAELSLQVEDRDMGDTARATRELSGGE
FREVSLALLALALSQMGGGGTPGGTLFIDEGFGALDAGSLDLAIDALETLQSGGRQVGV
ISHVERAMQARIATRAVREGGGSSERVEGFGV"
COMPLEMENT (16728. .17945)
                                              TATAQAQSAAQAARDRDGAWAALRAERAPLLDGQPTALHRSRFNDQRLAAQRAQOAAA
ADLATAQAALAAAEARAAETARAASEAATAQRAAEADLAAALEAAAMSAAELAALIAL
PPGTAERLRADLRGRDDAVTAARSALGARKTDLQEIEDQGNPAEDPEALSARLAALEA
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      TRLTEAERDKERLKRALLAHKGTRERLAVQQAETAQEAALAEARKTEAAARRDGLALA
LAPALARAGEDDPAAPGLAERLAATVSAVGAARTGLQAAQEALSALAPQLAAARRDSE
                                                                                                                                                                                                                                                            /product-"exonuclease SbcD homolog"
/protein_id="AAC16119_1"
/d_xref-"GI:3128267"
/translation="MRILHTADWHIGGTLNGWSREAEHRAFLADLGEILLAEQVDALL
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/protein_id="AAC16120.1"
/db_xref="G1:3128268"
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Pred. No. 6.9e-43;
0; Mismatches 543;
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/trans1_table=11
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Best Local Similarity 52.8
Matches 614; Conservative
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TSEDSLCRLYWRTALAIALGARHVLDAMERFGYAVETLHVTGGHVKNPLLMELYADVT
GKRIVVPATADAVLLGTAMTAATAGGVHASLAAAGAAMYPGNAEISGNPALAAHYERD
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GYLLGREFFEFAAMRFRSPADARLFRVKHRTTVFWAGLVIAAFLAVPFLNLLTPLFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLGSDNAAYVALMDYDPARTLLVIMDCGGNLLPLQRLSTTARKGGYRTLLITTRFYEW
GPESVDLCLAMPQSQNGGQGLLQLVSLLEFTLCALSAGADDAGKARYKNLAALKRSLR
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IDNFCGEVPKTREELVTLPGVCRKTANVVMSMAFGVPTLAVDTHVFRIANRLCLAPGK
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               GEPDTALHARIVARVTELRELEGEAFADRLHVLPDFHGNRSPLADPHAVGVVSGLTLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Atu4457"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="putative; ORF located using Glimmer"
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complement(5869. .6579)
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                                                                                                                              complement(4041. .4874)
/gene="Atu4454"
                                                                                                                                                                                        complement(4041. .4874)
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PKTVFGFIVAGLKARRDKDLQPFTVMSCDNIPHNGKVTKNAVVGLAALSDPAFANWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="conserved hypothetical protein"
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RAGNOFWUPVPDRYBEMKIRINGGHANARPARALDIHFVHFAMEHDLIARFLAKLE
KUBEIIPVIPPVPDRIANDFGELIERRFLANKIGDTIPRLAQDGSNRQPKFILDSTLDR
LSRGEDIVGLSLVSALWCRYFYGTSDSGKEIVFNDASAERLQAAAIKAKDDPVAFLAL
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DRFDIVWLDHRAIGEADRITASGHRVLDFAGNSVSPEWOMPKLAWIKTHMPQSWSRN
STRFDILADFLITWRATGSAQRNSVTQTRAKWNFLAAGLPBOWDAYLAFAGLDDLKFBAGL
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Chen, Y., Woo, L., Kitajima, J.P., Okura, V.K., Almeida Jr., N.F., Zhou, Y., Bovee Sr., D., Chapman, P., Clendenning, J., Deatherage, G., Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M., McClelland, E., Palmieri, A., Raymond, C., Rouse, G., Saenphimmachak, C., Ru, Z., Gordon, D., Eisen, J.A., Paulsen, I., Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M., Krespan, W., Perry, M., Gordon-Kamm, B., Liao, L., Kim, S., Hendrick, C., Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.
                                                                                                                                                                                                                                                                     Direct Submission
Submitted (27-SEP-2001) Department of Microbiology, University of
Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
98195-7742, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Agrobacterium tumefaciens str. C58 (U.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="mannitol 2-dehydrogenase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:180835"
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                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Atu4451"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1585. .2304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /qene="mtlK"
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                                                                                                                                                                                                                                             and Nester, E.W.
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JOURNAL
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1541 CAAGGATGTCATCCCGACCCTGAAGGCGCCTTCAGGCATGACGCTCGAAGGCTATCGGGA 1600
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                                                                                                                                                                                                                                                                                                                                                     1158 GCTGATCGAGCGCCGTTTCCTCAACCCGAAGATTGGCGATACCATTCCGCGCCTCGCGCA 1217
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/note="HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN GLPC-AIS
INTEREGENIC REGION"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-AUG-2001) Bioinformatics, Cereon Genomics, 45 Sidney
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linear chromosome, section 44
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                                                                                                                                                                                                                                                                                918 GCTCGAGAAAGCGGGGGTCCAGTTCGTCAAGGATGTTGCGCCCTACGAGCACATGAAGAT
                                                                                                                                                                                                                                                           CCGAATGCTCAATGCAGGCCATGTCATGCTCTGCTTCCCAGGCATTCTGGTCGGCTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGATCGGCGAAAATGTCGCCTTTCCGAATTCCATGGTCGACCGCATCACCCCCGCCAC
                                    1241 TTCGGCGGAAATCGCCAAGAAGCTCAACGCGGCCAGTGGGCTGGATGACGACCTGCCGCT
                                                                      CGGCGAGCGTGAACGCAATATCGCCCGTGACGATTTCGGCATCGAGGATAATTGGCCGGT
                                                                                                          GGTGGCCGAGGATTTCCATCAGTGGGTGCTGGAAGACCAGTTTGCGGATGGCCGTCCGCC
                                                                                                                                                                                   GCTTGAAAAAGCCGGCGTGCAGATGGTCGGGGACGTGACGGACTGGGAGTACGTCAAGAT
                                                                                                                                                                                                                                                                                                                                  1481 GAATGTGGATGACGCCATTGAAGACAGCGAACTCCTTGGCAATCTGAAGAACTATCTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 14945)
Hinkle,G., Slater,S.C. and Goodner,B.
Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Disease in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agrobacterium tumefaciens str. C58 (Cereon).
Agrobacterium tumefaciens str. C58 (Cereon)
Bacteria: Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Rhizobium:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Street, Cambridge, MA 02139, USA Approximately 800 bp of telomeric sequence missing from end of the chromosome and 200 bp missing from the right Location/Qualifiers
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/db_xref="taxon:181661"
98. .865
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Hinkle, G., Slater, S.C. and Goodner, B.
Direct Submission
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187 of the complete sequence.
AE008240 AE007870
AE008240.1 GI:15158760
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98. RFF
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738
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AUTHORS
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HDLEVTHEAMSPGEWKAKGGLTIRYGFHASPFGLALVMITDRGLAGCAFADFGDERA
CFEDMAGRWPNADYVEDREATAPYAAIIFEPAWTADKPLKYVLLGTDFÖVRVWKSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1060
                                                                                                                                                                                                                                                                                                                                                     translation="MNANIMLNEDITPIGSDYDTVRGVIELLTLDYREQPSLEAIAAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              941 CAACATCAACGAGGGACGGTGCGTTCGATCTGGAGAATGCGGCAGTAAAGGCCGACCT 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="identified by sequence similarity; putative;
located using Blastx/Glimmer"
                                                                                                                                                                                                                                                                                               /product="6-0-methylguanine-DNA methyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 11164;
 'product="conserved hypothetical protein"
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Pred. No. 3.8e-42;
); Mismatches 488
                                                                                                                                                                                                                                                                                                               /protein_id="AAL45253.1"
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ARKPECERCVIADICKSPEKTFDIPAPLVELPAQLFGAAGGE"
                                                                                                                                                                                               CFEDMAGRWPNADYVEDREATAPYAARIFEPAMWTADKPLRVVLLGTDFQVRVWKSLL
                                                                                                                                                                                                                        KIPMGRAVTYSNIACDIGQPTASRAVGAAVGANPVSFVVPCHRAVGKSGALTGYHWGL
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GYLLGREFFEFAAMRFRSPADARLFRVKHRTTVVFWAGLVIAAFLAVPFINLLTPLFAA
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GPESVDLCLAMPQSQORGQGLLQLVSLLEFTLCALSAGADDAGKARVKNLAALKRSLR
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5402. 6184
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/note="endonuclease III PA3495 {imported} - Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(6146. .6883) ...
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                                                                                                                                                                                                                                                                                                                                                                                      /note="hypothetical protein"
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7179. .8012
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/note="hypothetical protein"
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complement(4882, 5364)
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FDTQASITRAHIIASYKEGIERERILIKKASTWEGIRABETULGSEOTDKUITLES
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complement(3454...3690)
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CGLATLYDLAETLDLAIVSCGDIGPHSTSLSEGFISRETLRELVDAGCVCDTMFNFID
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                                                                                 /translation="MTDDDSERYRAPALDKGLDILELLARTDGGLTQIEIAKAIGKSP
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                                                                                                                                                                                                                                                                   complement(972. .1937)
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/gene-"AGR_L_814"
/gene-"AGR_L_814"
/note-"(AP001509) transcriptional regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="HYPOTHETICAL 11.0 KD PROTEIN Y4KP"
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/gene="^^
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/note="HVDO":-
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/gene="AGR_L_818"
complement(3743. .4615)
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                                                                                                                                                                                                          /gene="AGR_L_812"
complement(972. .1937)
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Rhodobacter sphaeroides operon regulator (smoC), periplasmic sorbitol-binding protein (smoC), periplasmic iner membrane protein (smoF), sorbitol/mannitol transport inner protein (smoG), sorbitol/mannitol transport inner membrane protein (smoG), sorbitol/mannitol transport inner membrane protein (smoG), sorbitol/mannitol transport ATP-binding transport protein (smoM), sorbitol/mannitol transport ATP-binding transport dehydrogenase (milk), and periplasmic mannitol-binding protein (smoM) genes, complete cds.

AF018073 L13697

AF018073.1 GI:2338757
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Schauder, S., Schneider K.H. and Giffhorn, F.
Polyol metabolism of Rhodobacter sphaeroides: biochemical characterization of a short-chain sorbitol dehydrogenase Microbiology 141 (Pt 8), 1857-1863 (1995)
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Schneider, K. H., Giffhorn, F. and Kaplan, S.
Cloning, nucleotide sequence and characterization
dehydrogenase gene from Rhodobacter sphaeroides
J. Gen. Microbiol. 139 (Pt 10), 2475-2484 (1993)
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TSFDSLCRLYWRTAIAIALGARHVLDAMERFCYAVETLHVTGGHVKNPLLMELYADVT
GKRIVVPATADAVLLGTAMTAATAGGVHASLAAAGAAMYPGNAEISGNPALAAHYERD
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                                                                                                                                                                              /db_xref="G1:15158771"
/translation="MMRQNLVAVDVGTASARAG1FDPAGRLLARSIHPILMQRPRENH
                                                                                                                                                                                                                                               DRFDTIVWLDHRAIGEADRLTASGHRVLDFAGNSVSPEMQMPKLMWLKTHMPQSWSRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11495 CAAGAACCCGTCCGCTCCGAAAACCGTGTTCGGTTTCATCGTTGCCGGGCTGAAGGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAATGTCGCCCCAAGGCCTTCCTCGGCTATGCGAAGGCGCGCGATCCGGAGTTGGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1181 GTGGATTGAGGAAAACGCGACCTTCCCGAACGGAATGGTTGATCGCATCACCCGACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1241 TTCGCCGGAAATCGCCAAGAAGCTCAACGCGGCCAGTGGGCTGGATGACGACCTGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGCGAGCGTGAACGCAATATCGCCCCGTGACGATTTCGGCATCGAGGATAATTGGCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Gaps
complement(8117. .9694)
/gene="AGR_L_826"
/note="D-ribulokinase (EC 2.7.1.47) - Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 259.2; DB 1;
Pred. No. 3.7e-42;
0; Mismatches 488;
                                                                                                              /transl_table=11
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                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                       tch 6.3%;
al Similarity 54.3%;
591; Conservative
                                                                       pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Si
Matches 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   821
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g ò g δ qq ò g ò Db ò qq Óγ g ò qq ò g ò q ò g

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AIFLMRMIGKNLDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LERLIAGLEDVSDGQIMIDGRDATEMPPAKRGLAMVPOSYALYPHMTVKKNIAPPLRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APFAMLFSDWTLQSYADVQERSNYARHFMNSVVISLGSTLVALAIAIPAWAMAFVPG
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TYSRAAPLTQFIASYSSPEGLFYAKLSAASTWAIAPILILGWFSOKQLVRGLTFGAVR
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YDRLFAINVSGTLFMMQAVARAMIAGGRGGKIINMASQAGRRGEALVGVYCATKAAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLTOSAGLNLIRHGINVNAIAPGVVDGEHWDGVDAKFADYENLPRGEKKRQVGAAVPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="ABC transporter; putative; formerly polk; SmoK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="sorbitol/mannitol transport inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="sorbitol/mannitol transport ATP-binding
       /note="ABC transporter; putative; SmoF"
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/gene="smog"
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GEDAPLLKDGFITPPEELTEMQDLGAVGEVAGWVFDSEGRYLETSINQRVAGVRVELSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFNAQHPDITVEWVTLEENVLRQKVTTDIATKGGCFDVLTIGTYEVPIWGKQGWLVSL
NDLPPEYDADDILPAIRNGLTVDGELYAAPFYGESSMIMYRKDLMEKAGLTMPDAPTW
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AWKATLTDYLDMMTNYGPPGASKNGFNENLALFQQGKCGMWIDATVAASFVTNPEEST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLVSRAISERLIHVRLEHRVSGCLHLEAALLRRFGLKLARVAPSLGSEVDPLPSIAPT
AAAEVERVLRSERPMVVAFGTGRSLRAIVEEMTSMVCEQHKIVSLNGNISADGSASYY
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EGWANVPPGTRTSLYENPEYQKVPFAKMTLDSINAADPTHPAVDPVPYVGVQFVAIPE
FQGIGTAVGQQFSAALAGSMSAEQALQAAQQFTTREMTRAGYIK"
                                                                                                                                                                                                 Direct Submission
Submitted (22-MAR-1996) Lehrstuhl fuer Angewandte Mikrobiologie,
Universitaet des Saarlandes, Geb. 2, Saarbruecken D-66041, Germany
                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (11-AUG-1997) Lehrstuhl fuer Angewandte Mikrobiologie,
Universitaet des Saarlandes, Geb. 2, Saarbruecken D-66041, Germany
On Aug 21, 1997 this sequence version replaced gi:1236173.
                                                                                                   fuer Angewandte Mikrobiologie,
2, Saarbruecken D-66041, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3061. .3088
/note="smoE-smoF intergenic region repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102. 3120
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                                                                                             Submitted (09-MAR-1994) Lehrstuhl Universited des Saarlandes, Geb. 6 (bases 4855 to 6162) Stein, M. and Giffhorn, F.
                       5 (bases 6163 to 8431)
Schneider, K.H. and Giffhorn, F.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:1063"
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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1687. 1692
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1731. 1727
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Stein, M. and Giffhorn, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Si-4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                            AUTHORS
TITLE
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PUBMED
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                                                                           TITLE
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Oy Db qq ò Db ŏ Pp οχ QΩ ò qq ò g ŏ Dp ò qq δ qq Óλ g δ g ò QQ ò

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1544 GGATGTCATCCCGACCCTGAAGGCGCCTTCAGGCATGACGCTCGAAGGCTATCGGGACAG 1603
                                        TGTGGATGACGCCATTGAAGACAGCGAACTCCTTGGCAATCTGAAGAACTATCTCAACAA 1543
                                                                                                                                                                                                     1604 CGTCATCAGCCGTTTCTCCAACAAGGCGATGTCGGACCAGACGCTCCGGATTGCTAGCGA 1663
                                                                                                                                                                                                                            7542 CATCCTGAACGGGGCCCATGCGGTGATCGCCTATCCGTCGGCGCTCATGGACATCCAGCT 7601
                                                             BCT 21-MAR-2001
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Escherichia.
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 10955)
Perna, NT., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,
Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A.,
Posfal, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L.,
Grotbeck, B.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K.,
Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,
Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome, contig 3 of 3, section
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7 Nature 409 (6819), 529-533 (2001) 21074935
                                                                                                                                                               7662 GGAGATCCTGCCCCATGTCCCGCCCGTGCCCGACACCAGCATCCCCGACTATCTTACCCT
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Submitted (22-OCT-2000) Laboratory of Genetics, University
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
/product="gluconate transport system permease 3"
/protein_id="AAG59503.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carbohydrates organic acids, alcohols" /note="Residues 1 to 447 of 447 are 100.00 pct to residues 1 to 447 of 447 from Escherichia co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .10955
/organism="Escherichia coli 0157:H7 EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /serotype="0157:H7"
/db_xref="taxon:155864"
/note="enterohemorrhagic"
complement(118 .1461)
                                                                                                                                                                                                                                                                                        1664 TGGCTGTTCCAAGGTTCAGGTGTTC 1688
                                                                                                                                                                                                                                                                                                                            7782 cecriceaacceecaecceaacric 7806
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Escherichia coli 0157:H7 EDL933
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AE005663.1 GI:12519330
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JOURNAL
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATTGAGGAAAACGCGACCTTCCCGAACGGAATGGTTGATCGCATCACCCCGGACCGTTTC 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATCTTGTTGATCCGGCCATCCGCATCGTTTCCATGACGATCACGGAAGGCGGCTACAA 943
                                                                                                                                                                                                                                                                                                                                                                                              644 TTTTCGAGCCCATGAGGCGTTCTACGTCGAGCAGATTCTTGAACACGCTCCGGACTGGGC 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTCGATGCCTCG --- GGCGCCTTCGATCCGACGCATCCCGATATCGTGGCCGCCGATGCGGC
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                                                                                                                                                                                                                                                                                                               TCCCCCCTATGACATCGACGGGATCAAGCCTGGGATCGTGCATTTCGGTGTAGGTAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6831 CTGGGCCATCCTCGCCGCGCGTCCCCCGACCGATGCGCGGATGCGCGAGGCTCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTCATGGGCGCCCTGCGTGACTATCTGCTTGCCCCGGCCGATCCGGAAGCCGTGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1004 GAACCCGGAAAAGCCGTCTACCGTTTTCGGTTACGTGGTCGAGGCCCTGCGTCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGATGCCGGTGGTAAGGCATTTACGGTCATGTCCTGTGATAACCTGCGTCATAACGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7245 TGTCACCCGCAACGCCGTGGTGGGCCTGGCCGAGCTCTACGACGCCGAGCTTGCGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1244 GGCGGAAATCGCCAAGAAGCTCAACGCGGCCAGTGGGCTGGATGACGACCTGCCGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7365 CCCGCA---CGAGCGCGAACTGGCGCAGGGCTTCGGCCTCGCCGATCCGGTGCCCGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1304 GGCCGAGGATTTCCATCAGTGGGTGCTGGAAGACCAGTTTGCGGATGGCCGTCCGCCGCT
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                                                                                                                                                                                                                                                                         Gaps
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ص
                                                                                                                                                                                                                                 Length 9810;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                       0; Mismatches 506;
                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                 Score 247.4; DB 1
Pred. No. 9.4e-40;
                                                                                                                  /gene="mtlK"
/EC_number="1.1.1.67"
/note="MtlK"
                       /gene="mtlk"
6680. .6684
/gene="mtlk"
/note="putative"
6691. .8124
                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                   6.0%;
                                                                                                                                                                                                                                                    53.4%;
        .8124
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                                                                                                                                                                                                                                 Query Match
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          gene
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                                              RBS
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gene

CDS

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/LEALALALON-WEMPLESNVLQSQIITDNHFLHHPKVESELTRKYERARLDTENIY
LLPLARGNNHNYDGKSVVEIRKLDISKESWPFNYVYTEACRESDGITTTGRMLYRNLKI
TSALDBIYGGGTGKRAHAATELAEGLENLFWKSPFDPVEDYTYVHEITLGFGCNVPGYA
GTTIGY ISTLPASQFKWTWTEOPPYDIYIDOIITVSGYANSSGFALAALLANLILGH
DPIIGIEAYPGTAEIHAKMGYKVIPGDEDAPLKRMTLQPSSCHPELFELKNGEWNYIGK
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/transl_table=11
/protein_id="AAGS9509.1" ...
/bx zef="c1:1519337"
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EMLYHDDEPLTFDLVWDNGGWRSATLENVS"
comptlement(7544 .. 8272)
/gene="YjiE"
                                                                                                                                                                                                                        /function="orf; Unknown function"
//note="Residues 1 to 276 of 276 are 93.47 pct identical to
residues 1 to 276 of 276 from Escherichia coli K-12 Strain
MG1655: B4325"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="WPPLOLSEOGKIFHSQIRHLLQQLESNLAELRGGSDYAQRKIKI
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FDHIRLFESQLFPVCASDEHGEALFDLVQPHFPLLNYSRNSYMGRLINRTLTRHSELS
                            NSMLVELFRQSWQWRENNPWMIQLHSHLDDSLYRKEWLGDHKQILAALIKKDARAAKL
AMWQHLENVKQRLLEFSNVDDIYFDGYLFDSWPLDKVDA"
complement(5656. .6486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Residues 1 to 133 of 133 are 98.49 pct identical to residues 1 to 133 of 133 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Residues 1 to 242 of 242 are 98.34 pct identical to residues 62 to 303 of 303 from Escherichia coli K-12 Strain MG1655: B4327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSTFFVSSMSELLKQVALDGCGIAWLPEYAIQQEIRSGQLVVLNRDELVIPIQAYAYR
MNTRMNPVAERFWRELRELEIVLS"
QLLESNIAEFAALQATREDIVKMRQALQLEERELASSAPGSSESGDMQFHLAIAEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MADYAEINNFPPELSSSGDKYFHLRNYSEYSEYTSGFFLSLMIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
/product-"putative transcriptional regulator LYSR-type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="putative regulator; Not classified"
                                                                                                                                                                                                                                                                                                                                                           /codon_start=1.
/transl_table=1.1
/product="corf, hypothetical protein".
/protein_id="AA659507.1"
/db_xref="GI:12519335".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="orf; Unknown function"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
/protein_id="AAG59508.1"
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/db_xref="GI:12519338"
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                                                                                                                                                                     complement(5656. .6486)
/gene="yjiC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(7544. .8272)
/gene="yjiE"
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                                                                                                                  /gene="yjic"
/note="25923"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5820. .6963
/gene="25924"
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/note="25925"
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/note="25927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="yjiD'
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NEMPYLDWTRTDLEYVLPDGSKALRFDOIEFAAFEMHILKRPGAEADYTEEEIAQAAE
RFATMSDEDSKALTRNIIAGLPGAEEGYTLDOFRKHLELYKDIDKAKLRENFAYFIKA
IIPVAEEVGVENAVHPDDPRPILGLEPRIVSTIEDMOWNDTVNSMANGFSWCTGSYG
VRADYDLVDMIKQFORRIYFHILKSTWREDDRTFHERAHLMODYDMYEVVKAIVEEE
HRRKAEGKEDLIPMRPDHGHOMLDDLKKKTNPGYSAIGRLKGLAEVRGVEAIQRAFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Residues 1 to 486 of 486 are 99.58 pct identical to residues 1 to 486 of 486 from Escherichia coli K-12 Strain MG1655: B4323"
                                                                               SVIIIGLIFGLAMFYEVAFIMLAPLVIVIAAFAKIPFLKLAIPAVAAATTAHSLPPPO
PGPVALVNAYGADMGMYIYGVLVTIPSVICAGLILPKFLGNLERPTPSFLKADQPVD
MNNLPSFGVSILVPLIPAIIMISTTIANIWLVKDTPAMEVVNFIGSSPIAMFIAMVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Residues 1 to 393 of 394 are 99.23 pct identical to residues 1 to 393 of 394 from Escherichia coli K-12 Strain MG1655: B4322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"mannonate, hydrolase"
/protein_id="AAG59504.1"
/db_xref="GI:LS59332"
/translation="MEQTWRWYGPNDPVSLADVRQAGATGVVTALHHIPNGEVWSVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MTTIVDSNLPVARPSWDHSRLESRIVHLGGGAFHRAHQALYTHH
LLESTDSDWGTGEVILMPGNBVLIFBLKRQQLLYTVARGAESTELKIIGSWKEALH
PELDGCGGILNAMARPQTAIVSLTYTEKGYCADAASGQLDLNNPLIKHDLENPTAPKS
AIGYIVBALRLRREKGLKAFTVWSCDNVRENGHVAKVAVLGLAQARDPQLAAMIEENV
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GAOFWADVVPFEMMKLRMLNGSHSFLAYLGYLGGYFTIADTWTNPDYRKAAFALMMQE
QAPTLSWPEGTDLNAYATLIERFSNPSLRHFTWQIANDGSQKLPQRLLDPVRLHLQN
GGSRRHLALGVAGWWRYTQGYDEGGRAIDVVDPMLAEFQKINQYGGADRVKALLGLS
GIFADDLPQNADFVGAVTAAYQQLCERGARECVAAL*
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                                                                                                                                                                     FVLFCTARGHDMOWVMNAFESAVKSIAMVILIIGAGGVLKOTIIDTGICDTIGMIMSH
GNISPYIMAMLITVLIRLATGGGVVSAMTAAGIISAAILDPATGQLVGVNPALLVLAT
AAGSNTLTHINDASFWLFKGYFDLSVKDTLKTWGLLELVNSVVGLIIVLIISMVA"
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VTRTVVREALIMLEIKGLVEVRRGAGIYVLDSSGSHNTDSPDANVCNDAGPFELLQAR
                   /translation="MHVLNILWVVFGIGLMLVLNLKFKINSMVALLVAALSVGMLAGM
DLMSLLHTMKAGFGNTLGELAIIVVFGAVIGKLMVDSGAAHQIAHTLLARLGLRYVQL
                                                                                                                                                                                                                                                                                                                                                                                                                    /function="enzyme; Degradation of small molecules: Carbon compounds"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="enzyme; Degradation of small molecules: Carbon
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/protein_id="AAG59505.1"
/db_xref="G1:1251933"
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/db_xref="G1:12519334"
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/gene="uxuA"
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/gene="uxuA"
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/gene="uxuR"
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/gene="uxuB"
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/gene="uxuR"
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H7 DNA, complete genome, section 20/20.
1097 GTACGGACCTGAACGCCTATGCGACGCTGCTGATCGAGCGTTTCAGCAACCCGTCTCTGC 4156
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Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sub_strain:RIMD 0509952)
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iishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
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Yutsudo, C.H., Kurokawa, K., Ishii, K., Hattori, M., Abe, H., Iida, T.
Yamamoto, K., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae:
Escherichia
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Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                     1217 ACCCGGTGCGTCTGCACCTGCAAAACGGCGGCAGCTGGCGTCACCTGGCGCTGGCGTGG
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orv strain K-12
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                                                                  CGGACCAGACGCTCCGGATTGCTAGCGATGGCTGTTCCAAGGTTCAGGTGTTTTGGACGG
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0157:H7 and genomic comparison with a laboratory
DNA Res. 8 (1), 11-22 (2001)
21156231
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Genes Genet. Syst. 74 (5), 227-239 (1999)
20198780
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Hayashi,T.,
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REDVEYDGMGTYREDPANGEDGDDETVDEDDDGVRH"
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YAGDARNNWGNSMLEAAALTGLDLRIX-YAPQACWBEAALVTECRALAQONGGNITTIFED
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complement(4746. .5039)
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Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamaddoka, Sulta, Osaka 565-0871,
Japan (E-mail:kenégen-info.osaka-u.ac.jp,
URL:http://www.gen.info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="identical to B4250_ECOLI gi|1790699 (Conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to YJGJ_ECOLI gil1790700 percent identity 92 in 84 aa (Conserved in E.coli K-12)"
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                                                                                                                                                                                                   Location/Qualifiers
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RKMITAQLIYYFGIAVSTSYLTVSLRNHFMSNLSLNDGRIRFRSTLTYHGMLYRMCAL
VVISGITGGLAYPLLKIMMIDWQAKNTYLLGDLDDLPLINKEEQPDKGFLASISRGIM
                                                                              675
                                                                                                                                                                                            ACGACCGCGTGCTGAAAAACCTGAAAAAACAGCAACTGCTGTACACCGTGGGGAAAA
                                                                                                                                                                                                                                                                                                                                                                        616 GGATCGTGCATTTCGGTGTAGGTAACTTTTTCGAGCCCATGAGGCGTTCTACGTCGAGC
                                                                                                                             GTTCAAAGAAAAAGCCGAGGAATTCAAGGCCCAGGACTGCCTGTATTCCCTGACCGAGA
                                                                                                                                                                                                                      CCCCGGCCGATCCGGAAGCCGTGCTGAAGCATCTTGTTGATCCGGCCATCGCTTT
                                                                                                                                                                                                                                                                                                               CCATGACGATCACGGAAGGCGGCTACAACATCAACGAGACGACCGGTGCGTTCGATCTGG
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                                                       0; Mismatches 612;
                                  DB 1;
                                Score 236.8; DB 1
Pred. No. 9.6e-38;
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RME603647 189333 bp DNA linear BCT 05-JUL-2002
Rhizobium meliloti (Sinorhizobium meliloti) 1021 complete pSymB;
segment 6/6.
AL603647 AL591985
AL603647.1 GI:15141286
                                                                                                                                                                                             79067 GTACGGACCTGAACGCCTATGCGACGCTGCTGATCGAGCGTTTCAGCAACCCGTCTCTGC 79126
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/protein_id="CAC49799.1"
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The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium mellioti
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9889-9894 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sinorhizobium meliloti.
Sinorhizobium meliloti
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                AAACCGTGCGTCGGGCGATCGAAGACAAGCGGGACCTGTCACGTATAGCGTTCGGAATTG
                                                                                                                                                                                                                                                                          CATCCTATCTCGAAATGCTGCGTGGTCGCGACGAGAAGGGCGGGACGTATGAATCGTCCG
                                                      CGGACCAGACGCTCCGGATTGCTAGCGATGGCTGTTCCAAGGTTCAGGTGTTCTGGACGG
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/strain="1021"
/db_c="taxon:382"
/plasmid="pSymb"
complement(126. 932)
/gene="idnol or SMb20692"
/gene="idnol or SMb20692"
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1. .189333
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EEVLTGANEAIETFAAQSAEYGKLVGRSAGGLPAKPRLLSFQELRAAAARVFGHGFDA
FYAEKEREFAQSDNPLVATRQLTEWLVGIARLSGPAIVIGFSGLHYPPSHLRLAEGND
RSLHQAIEKARAGLGNDPARSLIWKPHFYGISDMSFLGLAASGSQVVSDNTPISRLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDVTSDQGDGSEGRAVYAGTIGKLLPPALVIGGSSHASYPFEGVSAQAMAAGILARLE
GNASLADRDDNDISPPPICLEAKDLRDGYEVTTPERFWIAFNWLYHSWTADALFERFR
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agwtwaresgaastdnayvrgdvtslapkvagyvtaveveddngavragdvlfriddrd
yraklaqavanveaaearltnvdaemalqualirqaeaqqrrsvvaelnlaakaydrrr
AEILVKATDIFGSQAEAEQWLERPAVGLDQRRPIDLLGTPPGVELVEDHLDRLEYGIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mtnagEETVSRAGSRIDSERVRQFALRMTSWPSETGTPGEASFA
DRLHGLLGELPYFREHPQDLGLLASHGEPLTRNVVALVRGTGKRTLVMAGHFDTVSTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYHELKALACDSLALKDALIESLSARTGRSEQEERALQDLASGDFLPGRGLLDMKSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVAIACLEQFAADTDROGNLMLVATPDEERESRGMRSLRDALPGLVRDFDIEIAGGIN
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IGDTYATPDEFAWLDVGYTTFKLIGFWAASWLMSRFDPRNLVVGSTLAMGMACGIAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TARLDLLVALRMIQGFSGGTLLVGGQAIIFLTFPHSRQPLLQAFFAMGSVVAPATIAP
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CFAFIVSFVAGAALFGSAFLIPSFAVSVLAFTPTDAGQLLLPSGALFIGALLIAAFLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLRRVPPVATVPFGILMIMAAMWMLSGSTSESGAGDMMAAILLRGAGLGFLFLSITLI
AFSNLNSRNLASGIGLFNTGRQLGGLIGVSALQTLIEHNVSHNLAVLGANVTAGAPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative protein secretion protein, HlyD family, similar to E. coli EmrK" /protein_id="CAC49806.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADRLTTTAALLTAKGMDAAAASRGAASLLGRAVAGQSTVIAFDTAFNAIGLLFVIAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPSENALRFPTVNLGPWGREFHQKFERVHEPYAFRVLPELVSEIARTFLGDDRHRD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of small molecules"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, similar to E.
                                                                                                                                                                                   Macromolecule
                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative peptidase, similar to arginine
                                                                                                                                                                             /function="MACROMOLECULE METABOLISM; Macromolec degradation: degradation of proteins, peptides, glycopetides. Product confidence : putative Gene name confidence : hypothetical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLVGIKIGLARYAKARAEKGRAGVAAKPSGHHTLPIKRVPAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4701..6353)
/gene="SNAD20698"
/ogene="SNAD20698"
/gene="SNAD20698"
/function="CELL PROCESSES; Transport
/functe="Product confidence : putative
Gene name confidence : putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative transport
multidrug resistance protein
/protein_id="CAC49805.1"
/db_xref="GI:15141293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, peptide secretion"
/note="Product confidence :
                                                                                                                                                                                                                                                                                                                                                                                                                                                              utilization protein RocB"
/protein_id="CAC49804.1"
/db_xref="G1:15141292"
/db_xref="SPTREMBL:Q92TU1"
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/db_xref="SPTREMBL:092TT9"
                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
/transl_table=11
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/gene="SMb20699"
                                                             .4549)
                                                                                                                      complement(2855.
/gene="SMb20697"
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OSELARPSIAPYAASKGGLKMLTKGMALDWGRYGIRVNGLAPGYFKTELNSALVSDEK
STWILEORTPLGKWGDTGELAAAAVFLASAASSFVTGHILYVDGGITSCL"
COMDlement (1063 . 1361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MGADGDFWAALDARMRVRVIERLRVADMSAVPDINAGNTNAPAT MLGNRCAGFILGTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MTLLPVALGGTELVAWRLDQAVHAPTWDSGEGAYRVGGRWNSKG
VRAVYCSLDPATAILEVAVHKGFRALDWVAHTWTAAAIADAGDVYVVDPKSVPNPNWA
RPGIPGAGQQAYGDDLLRRHRFVAIPSAVSPHSWNLVFLGGAAPAAYALKFQEPFALD
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                                                                                                                                                                                                                                                                                                                          /function="MISCELLANEOUS; Hypothetical/Partial homology"
/note="Product confidence : hypothetical
Gene name confidence : hypothetical
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/note="Product confidence : hypothetical
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/protein_id="CAC49802.1"
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/gene="SMb20695"
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/gene="SMb20696"
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/qene="SMb20694"
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ELIRSETISQAHVDESDAAKSRAEANVLAASATVEAQQQRIAVLAAQREAAVAAVAQA
EAARDLAGIDLESTVVRAPVGGVIGNRQVRVGRLVAPGASLLDIVPLDNVWIVANFKE
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                                             Length 189333
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                                                                           0; Mismatches 618;
                                              DB 1;
                                             Score 236.2; DB 1 Pred. No. 1.3e-37;
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                                      CCTGAAGGCGCCTTCAGGCATGACGCTCGAAGGCTATCGGGACAGCGTCATCAGCGTTT
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D-sorbitol dehydrogenase; SLDH; L-sorbose production; NADP+ dependent; sorbitol; mannitol; arabitol; oxidation; 2-keto-L-gluconic acid; L-ascorbic acid biosynthesis; vitamin C; ds.
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Takata Y;
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/SIDS2/gcgdata/geneseq./geneseqn.embl/NA1992.DAT.
/SIDS2/gcgdata/geneseq./geneseqn.embl/NA1993.DAT.
/SIDS2/gcgdata/geneseq./geneseqn.embl/NA1993.DAT.
/SIDS2/gcgdata/geneseq./geneseqn.embl/NA1994.DAT.
/SIDS2/gcgdata/geneseqn.embl/NA1995.DAT.
/SIDS2/gcgdata/geneseqn.embl/NA1996.DAT.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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DNA sequence of hu 88421nt genomic DN Spinocerebellar at

Rhizobium species Rhizobium species

culturing its gene-transformed host cells, useful for producing L-sorbose or 2-keto-L-gluconic acid as an intermediate in L-ascorbic Gluconobacter oxydans derived D-sorbitol dehydrogenase obtainable by acid production

Claim 9; Page 60-63; 72pp; Japanese

CalbH: AAR2172) and to the gene encoding it (AAA97430). SLDH has a molecular weight of about 54 Kba and catalyses the conversion of D-sorbitol into L-sorbose using NaD+ as a co-enzyme. SLDH specifically catalyses the oxidation of sorbitol, mannitol and arabitol, but does not act on xylitol, ribitol, inositol and glycerol. The invention also act on xylitol, ribitol, inositol and glycerol. The invention also concompasses expression vectors and host calls comprising the concombinater oxydans SLDH gene, and the recombinant production of SLDH. The invention further relates to a method for preparing L-sorbose by contacting the recombinant SLDH with D-sorbitol; a process for producing 2-keto-L-gluconic acid by contacting recombinantly produced sorbose dehydrogenase and/or sorbosone dehydrogenase with L-sorbose; and a propersion from 2-keto-L-gluconic acid or its alkaline earth metals salts by conversion from 2-keto-L-gluconic acid. SLDH is useful for producing L-sorbose or 2-keto-L-gluconic acid as an intermediate in L-ascorbic invention relates to Gluconobacter oxydans D-sorbitol dehydrogenase production. The present sequence represents the Gluconobacter

Sequence 4115 BP; 833 A; 1133 C; 1270 G; 879 T; 0 other;

ö 120 180 240 300 420 420 480 540 540 009 181 GGCACATAGTTGCGAGGAGTTGCGCGCAAAGCAGAACCAGCATGAACAGCAGCACTCCGA 240 TITIGIGATGICCCIGIICCGCGAGGATCICGAACGGGCTGIIGGGGGTGCTCAIGCGTIC 360 9 9 GATGCGGCGTCTGTTGACCGACATGATGCTGGTGGCACGTGCCATTGCGACGGGGCGTGC 241 AGACGAGGAAATCCTCGGCCTCCTACCGCGATTGGAAGAGCAGACCCGTCCTGAGATGCG 1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCGGTTTTGGCAGCGCTCCCTAGATT 1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCGGTTTTGGCAGCGCTCCTAGATT GACCGGGAACACACGCCTGCTGCTTTGTACAAGGGGCTGAGTCATGCGCTGCGTGGGCT 121 GACCGGGAACACAGGCCTGCTGCTTTGTACAAGGGGCTGAGTCATGCGCTGCGTGGGCT GGCACATAGTTGCGAAGAGCAGTTGCGCGCAAAGCAGAACCAGCATGAACAGCAGTCCGA TGATGCGAGTGCCGCAAAAGGTCTCTGAACAGGACGTCCCGCGGAGGGCCAGTCAGAGGTC GAAATGGCTCCTGTTGAAACCGTCATTCGGTTTTTTACGTTGTTTCGGGGCTATGATGGCA CATGCCCGGCCTTGTCGGTCCCCGTCAGCGACCGGCCCGAAACCACGGAGAATTCCATGA TTACGCGCGAAACCCTTAAGTCTCTTCCTGCCAATGTCCAGGCTCCCCCTATGACATCG Gaps DB 21; Length 4115; ; 0 Indels .; 0 .100.0%; Score 4115; 100.0%; Pred. No. 0; ative 0; Mismatches Best_Local Similarity 100. Matches 4115; Conservative Query Match 61 61 121 181 301 301 361 421 481 рp q δ qq g q g Ω δ g ò δ ò õ g ò δ Db õ

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1 ACGGGATCAAGCCTGGGATCGTGCATTCGGTGTAGGTAACTTTTTTGAGCCCATGAGG	7	CGTTCTACGTCGAGCAGATTCTTGAACACGCTCCGGACTGGGCGATTGTTGGTTG	1 TGACGGGCAGTGACCGTTCAAAGAAAAAGCCGAGGAATTCAAGGCCCAGGACTGCTGT 	-	1 ATTCCCTGACCGAGACGCCTCCGTCCGCCAAGAGCACGGTGCGCGTCATGGGCCCCTG	1 GTGACTATCTGGTTGCCCCGGCCGATCCGGAAGCCGTGCTGAAGCATCTTGTTGA	1 GTGACTATCTGCTTGCCCCGGCCGATCCGGAAGCCGTGCTGAAGCATCTTGTTGATCCG	1 CCATCGGCATGGTTTCCATGACGATCACGGAAGGGGGGTACAAAAATCAACGAAGGGGACG 1	1 GTGCGTTCGATCTGGAGAATGCGGCAGTAAAGGCCGAACTCAAGAACCCGGAAAAGCCG	1 GTGCGTTCGATCTGGAGAATGCGGCAGTAAAGCCGACTCAAGAACCCGGAAAAGCCGT	1 CTACCGTTTTCGGTTACGTGGTCGAGGCCCTGCGTCGTTGGGATGCCGGTGGTAAGG	1 CTACCGTTTTCGGTTACGTGGTCGAGGCCCTGCGTCGTCGTTGGGATGCCGGTGGTAAG	1 CATTACGGTCATGTCTGTGATAACCTGCGTCATAACGGCAATGTCGCCCGCA	1 CATITACGETCATGTCCTGTGATAACCTGCGTCATAACGGCAATGTCGCCCGCAAGGC	1 TCCTCGGCTATGCGAAGGCGCGCGATCCGGAGTTGGCGAAGTGGATTGAGGAAA	1 recrederardedaaddegeeceareegaartegeeaagregarraagaaaaaeeeg	1 CCTTCCCGAACGGAATGGTTGATCGCATCACCCCGACCGTTTCGGCGGAATCG	1 CCTTCCCGAACGGAATGGTTGATCGCATCACCCCGACCGTTTCGGCGGAAATCGCCAAG	1 AGCTCAACGGGCCAGTGGGCTGGATGACGACCTGCCGCTGGTGGCCGAGGATTTT	1 AGCTCAACGCGGCCAGTGGGCTGGATGACGACCTGCCGCTGGTGGCCGAGGATTTCCAT	1 AGTGGGTGCTGGAAGACCAGTTTGCGGATGGCCGTCCGCCGCTTGAAAAAGCCGGCGTGC 	1 AGATGGTCGGGGACGTGACGGACTGGGAGTACGTCAAGATCCGAATGCTCAATGCAGGG	1 AGATGGTCGGGGACGTGGCTCGGACTGGACGTCAAGATCCGAATGCTCAATGCTAATGCTCAATGCTAA		1 ATGTCATGCTCTGCTTCCCAGGCATTCTGGTCGGCTATGAGAATGTGGATGACGCCATT	-	1 AGGACAGCGAACTCCTTGGCAATCTGAAGAACTATCTCAACAAGGATGTCCTCGGACC	1 TGAAGGCGCCTTCAGGCATGACGCTCGAAGGCTATCGGGACAGCGTCATCAGCGTTTCT	1 TGAAGGCGCCTTCAGGCATGACGCTCGAAGGCTATCGGGACAGCGTCATCAGCCGTTTC	1 CCAACAAGGCGATGTCGGACCACGACGCTCCGGATTGCTAGCGATGGTGTTCCAAGG	1 CCAACAAGGCGATGTCGGACCAGACGCTCCGGATTGCTAGCGATGGCTGTTCCAAGGTT	1 AGGIGTTCTGGACGAAACCGIGCGTCGGGCGATCGAAGACAAGCGGGACCTGTCACGTA
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597 ATCGACGGGATCAGCCTGGGATCGTGCATTTCGGTGTAGCTATTTTCGAGCCCAT 656	837 CTGCGTGACTATCTGCCCCGGCCGATCCGGAGCCGTGCTGAGGCATCTTGAT 896	957 ACCGGTGCGTTCGATCTGGAGAATGCGGCAGTAAAGGCCGACCTCAAGAACCCGGAAAAG 1016	1077 AAGGCATTTACGGTCATGTCCTGTGATAACCTGCGTCATAACGGCAATGTCGCCCGCAAG 1136	1197 GCGACCTTCCCGAACGGAATGGTTGATCGCATCCCCGACCGTTTCGGCGGAAATCGC 1256		1557 ACCCTGAAGGCGCCTTCAGGCATGACGCTCGAAGGCTATCGGGACAGCGTCATCAGCCGT 1616 11111111111111111111111111111
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Oy 3901 CATCAGGGTCCGGATCACCAGCAGGAGGATATAAGCGACGGTCGGCCG 3960 11111111111111111111111111111111111	RESULT 2 AA235672 ID AA235672 standard; DNA; 1458 BP. XX AC AA235672; XX DT 27-JAN-2000 (first entry)	XX DE Gluconobacter suboxydans L-sorbose reductase nucleotide sequence. XX KW Gluconobacter suboxydans; L-sorbose reductase; genetic engineering; XX XX XX XX XX XX XX	FH Key Location/Qualifiers FT CDS 1.1458 FT /*tag= a FT XX NAU9920390-A. XX PD 23-SEP-1999.	XX PF 11-MAR-1999; 99AU-0020390. PR 13-MAR-1998; 98EP-0104546. XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F. XX PI HOShino T, Tazoe M, Shinjoh M, Kon T; XX		SQ Sequence 1458 BP; 329 A; 386 C; 434 G; 309 T; 0 other; Query Match 23.2%; Score 955.6; DB 20; Length 1458; Best Local Similarity 78.5%; Pred. No. 4.5e-241; Matches 1144; Conservative 0; Mismatches 314; Indels 0; Gaps 0; Qy 537 ATGATTACGCGCAAACCCTTACGTCCTGCCAATGTCCAGGCTCCCCCTATGAC 596.

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CGTATAGCGTTCGGAATTGCATCCTATCTCGAAATGCTGCGTGGTCGCGACGAGGAGGGC 1796
                                                                                                                                                                                                                                                            TCCGAACTGGATCAAAAGGTCATCGTGCTGCGGAAGATCATCCGCGAAAAGGGCGTAAAA 1976
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GTTCAGGTGTTCTGGACGGAAACCGTGCGTCGGGCGATCGAAGACAAGCGGGGACCTGTCA 1736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                     GACGACTTCGAAAGCTCTCTGAAGCTCCCGGCGTTCGATGGGTGGCGCGATCTGGATACG
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(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
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28-AUG-1998;
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                                                                                                                                                                                                                                                                                                              643
           macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acte conditions. The products can also be used for detection and diagnosis. AAX32002 to AAX320080, and AAY49503 to AAX49511 represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGGCCATCCTCGGCGCGGGGGTCCGCCCGACGGATGCGCGGAGGCTCTGGC
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                                                                                                                                                                                                                                             Length 9810;
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endometrial bleeding disorders, diabetic retinopathy,
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BETH ISRAEL DEACONESS MEDICAL CENT
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99US-0144882.
99US-0147823.
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FORNWALD J A.
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                                                                                                                                                                                                          The present invention relates to human METH1 and METH2, (ME for metalloprotease and TH for thrombospondin; see AABS0002 and AABS0003). The present sequence is an expressed sequence tag (EST) for METH. METH can be used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease. Theumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, oronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler Webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, theromosclarosclarosis. METH can also be used in birth control. METH can also be used in birth control. METH can also
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METH1 and METH2 polynucleotides and encoded polypeptides, inhibit angiogensis in the treatment of disorders such as rheumatoid arthritis and psoriasis -
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Pred. No. 2.8e-54;
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GGCGGAAATCGCCAAGAAGCTCAACGCGGCCAGTGGGCTGGATGACGACCTGCCGCTGGT
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Ikeda M, Ozaki A;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, in the examplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGAAGGCGCCTACAACATCAACGAGACGGACGGTGCGTTCGATCTGGAGAATGCGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1509 BP; 341 A; 474 C; 376 G; 318 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 213.6; DB 22;
Pred. No. 9.6e-46;
); Mismatches 609; I
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Matches 617; Conservetting
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                                                                                                                                   TCCTTGGCAATCTGAAGAACTATCTCAACAAGGATGTCATCCCGACCCTGAAGGCGCCTT 1572
                                                                                                                                                  CAGGCATGACGCTCGAAGGCTATCGGGACAGCGTCATCAGCCGTTTCTCCAACAAGGCGA 1632
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                                          AGGATGCCTTCACCCAGGGCCGCCCCCGCGTACGAGGAGGTTGGCGTGCAGGTCGTCTCCG 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:335
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                                                                                                 TGTCGGACCAGACGCTCCGGATTGCTAGCGATGGCTGTTCCAAGGTTCAGGTGTTCTGGA
                                                                                                                                                                                                                                                                      TCAAAGACACCGTACCGCGCCTGTGTGCGGAATCCTCCGACCGCATTCCAAAGTGGCTGT
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ARATALISO TO ANALYJSO THOOGHOUSE CHE COLYMBOATE CHAIN STUTE ANALYJSO TO ANALYJSO THOOGHOUSE CHE COLYBRACKER TO ANALYJSO THOOGHOUSE THE CALL ANALYSO TO ANALYJSO THE C. Glutamicum SNP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a protechnogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a uncleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a coffactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (II) encoded by them are used for diagnosing the presence or activity of corpebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to nost cells in evolutionary studies, in determining SMP protein regions required function, in modulating sMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 213.6; DB 22; Length 1632;
Pred. No. 1e-45;
); Mismatches 609; Indels 18;
                                                                                                                                                                                                                                                                                                                 Haberhauer G;
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99US-0151572.
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                                                                                                        AAATCGGCTACATCGATGCGTGGCTGCCAGTTTCTGAAGATTTCACCCAATGGGTCCTCG
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                  CGGAAGCCGTGCTGAAGCATCTTGTTGATCCGGCCATCGCTTTCCATGACGATCA
                            CGGAAGGCGGCTACAACATCAACGAGACGACCGGTGCGTTCGATCTGGAGAATGCGGCAG
                                                                          CTGAAGGCGGATACAACATCGATCCGGCGACAGAAGATTTCGACCACCACCATCGAA
                                                                                                                                  GTTACGTGGTCGAGGCCCTGCGTCGTTGGGATGCCGGTGGTAAGGCATTTACGGTCA
                                                                                                                                              TGTCCTGTGATAACCTGCGTCATAACGGCAATGTCGCCCGCAAGGCCTTCCTCGGCTATG
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AAH64966 standard; DNA; 349980

AAH64966/c

AAH64966;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of nucleotide and protein agequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and manalysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium activity a nomologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, saccharides and organic acids, particularly Liysine. The present sequence is a nucleic acid described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAAGAGCACGGTGCGCGTCATGGGCGCGCGCGTGACTATCTGCTTGCCCCGGCCGATC
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49.6%; Pred. No. 1.1e-44;
tive 0; Mismatches 609; Indels 18; G
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amino acid synthesis; vitamin; saccharide
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Senoh A, Ikeda M, Ozaki A;
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2000JP-0159162
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                            organic acid synthesis; ds.
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Coryneform bacterium;
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Matches 617; Conserv
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07-APR-2000;
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forensic;

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
DNA encoding novel human diagnostic protein #28804.
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                                                                                         -ACCGTTTTCG 1032
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                                                                                                                                                                                            CGGAAGCCGTGCTGAAGCATCTTGTTGATCCGGCCATCCGCATCGTTTCCATGACGATCA
                                             CGGAAGGCGGCTACAACATCAACGAGACGACCGGTGCGTTCGATCTGGAGAATGCGGCAG
                                                                                                              121987 TCGTTGCTGACCGCGAAGCCCTGCAGGCGGCGGTACTTCCACTTTGCAGACCTTCTTTG
                                                                                                                                                                               TGTCCTGTGATAACCTGCGTCATAACGGCAATGTCGCCCGCAAGGCCTTCCTCGGCTATG
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AAS93000 standard;

AAS93000 RESULT

13-FEB-2002

AAS93000;

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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, colourers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques control or control or generating antibodies against it, detecting or quantificating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of companion and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human DNA and and confidence other types of data and products dependent on DNA and and annother sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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Pred. No. 1.6e-20;
); Mismatches 331; Indels 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 28804; 103pp; English.
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                                                                  2000US-0540217.
2000US-0649167.
30-MAR-2001; 2001WO-US08631
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                                                                                                                    ATGCGGCAGTAAAGGCCGACCTCAAGAACCCGGAAAAGCCGTCTACCGTTTTCGGTTACG 1038
                                                                                                                                                                                              GTGATAACCTGCGTCATAACGGCAATGTCGCCCGCAAGGCCTTCCTCGGCTATGCGAAGG 1158
                                                                                                                                                                                                                                                    3083 AGCGTTCGCCAGAACTCGCCGGGTGGATAAAAGAGCACGTCAGTCTTCCGGGAACCATGG 3142
                                                                                          CGGCCGATCCGGAAGCCGTGCTGAAGCATCTTGTTGATCCGGCCATCCGTTTCCA
                                                            2783 TGGATTCCTTAGCGGCAATTATTGAGAAATTTTGCGAGCCACAGGTGGCAATTGTTTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                             novel human diagnostic protein #29688.
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymocleotides are also used in disponsitics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II): (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymocleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      682 T---TGAACACGCTCCGGACTGGGCGATTGTTGGTGTTGGCCTGACGGGCAGTGACGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.
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0; Mismatches 331; Indels
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                                                                                                  TCCCCTATGAAGAGGCGAAGATTCGCATTCTTAACTCTTCACAGTTGCATCGCCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            682 TTGAACACGCTCCGGACTGGGGGATTGTTGGTGTTGGCCTGACGGGCAGTGACCGTTCAA 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAAAAAAGCCGAGGAATTCAAGGCCCAGGACTGCCTGTATTCCCTGACCGAGACGGCTC 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a positive selection system that involves conferring to transferred cells the ability to metabolise arabitol, ribition and/or mannitol. The positive selection method is used in positively selecting transgenic cells from a population of cells Using the positive selection method, the presence of the gene of interest in the genetically transformed cells may be determined without the disadvantages associated with traditional negative selection of the transformed cells is achieved without directly damaging the neighbouring non-transformed cells is achieved without transformed cells may be identified by simple visual means without the use of a separate assay to determine the presence of a marker gene. This technique also avoids the release of antibiotics or other dangerous genes into the environment. The present sequence is Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Positively selecting transformed cells comprising selectable marker gene and desired gene, from a cell population by using marker compounds e.g., arabitol, ribitol which confer selective advantage on transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     622 IGCATTTCGGTGTAGGTAACTTTTTCGAGCCCATGAGGCGTTCTACGTCGAGCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                              mannitol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1848;
                                                                                                                                                                                                                                                            Positive selection system; metabolise; arabitol; ribitol; transgenic cell; marker gene; arabitol dehydrogenase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1848 BP; 494 A; 443 C; 473 G; 438 T; 0 other;
                                                                                                                                                                                                                       Escherichia coli strain C arabitol dehydrogenase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105; DB 22; Dred. No. 4.1e-17; O; Mismatches 560;
    248 TCGACCGCATTGTTCCGGCTGCAACCGACGAA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain C arabitol dehydrogenase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 34-35; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kane P;
                                                                                                      AAD16810 standard; DNA; 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.6%;
46.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2001; 2001WO-US07474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0188291
2000US-0255595
                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lafayette P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-565596/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 509; Conserv
                                                                                                                                                                                                                                                                                                                      Escherichia coli C.
                                                                                                                                                                                                                                                                                                                                                               WO200166779-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2000;
15-AUG-2000;
                                                                                                                                                                                  29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parrott W,
                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2001
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                                                                                                                                             AAD16810;
                                                               RESULT 10
AAD16810
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AAS78056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS care used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes from FF cells allows the production of polanes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be dentified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore control of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore confined to microarrays based on function of the gene products to facilitate microarrays based on function of the gene products to facilitate analysis of the results. AAF11248 to AAF11247 represents ESTS from Aspergillus or AAF14879 to AAF1887 represents ESTS from Aspergillus or AAF14879 to AAF1887 represents ESTS from Aspergillus or all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1160 GCGCGATCCGGAGTTGGCGAAGTGGATTGAGGAAAACGCGACCTTCCCGAACGGAATGGT 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1220 TGATCGCATCACCCCGACCGTTTCGGCGGAAATCGCCAAGAAGCTCAACGCGGCCAGTGG 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1280 GCTGGATGACGACCTGCCGCTGGTGGCCGAGGATTTCCATCAGTGGGTGCTGGAAGACCA 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 CATCGAGGACTCGTGGCCCGTCGTCAGAGCCCTTTATGCAGTGGGTAATTGAGGATCA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
                                   Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GCGCAACCCCGAGATCGCGAAGTGGATTGCCGAACAGGGCGCCTTCCCCAACGCCATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olsen PB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Kauppinen S, Clausen IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 88; Page 2202-2203; 3161pp; English.
Aspergillus oryzae EST SEQ ID NO:5276.
                                                                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shuster JR,
                                                                                                                                                                                                                                                                                                 22-MAR-2000; 2000WO-US07781.
                                                                                                                                                                                                                                                                                                                                         99US-0273623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-594572/56
                                                                                                                                                                    Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rey MW,
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                                                                                                                                                                                                            WO200056762-A2.
                                                                                                                                                                                                                                                                                                                                         22-MAR-1999;
                                                                                                                                                                                                                                                       28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berka RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noté: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
1340 GITTGCGGATGCCCGTCCCCCCTTGAAAAGCCGGCGTGCAGATGGTCGGGGGACGT 1396
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                      forensic;
                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2810 BP; 696 A; 699 C; 758 G; 657 T; 0 other;
                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #13860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 70.6; DB 23;
Pred. No. 5.6e-08;
); Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                   BP.
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                                                                                                                                 AAS78056 standard; cDNA; 2810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                            (first entry)
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Best Local Similarity 47.7
Matches 239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Claim 86; Page 647; 3161pp; English.
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    \overset{\circ}{\mathcal{A}} \times \overset{\circ}{\mathcal{C}} \circ \overset{\circ
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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FP cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes conditions of use fluorest conditions of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production contential of the microorganisms to be improved. New genes may be contential of the microorganisms to be improved. New genes may be consisted undersome copy number variation and stability can be consisted to changes in culture conditions, environmental stress, spore monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore componensis, recombination, metabolic or catabolic pathway concernays based on function of the used and organisation of the range conditions of undersome consisting elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the malysis of the results. AAF07478 to AAF11248 to AAF11248 to AAF11248 to AAF11248 to AAF11247 represents ESTS from AAF14879 to AAF1537 represents ESTS from Aspergillus oryzae; and AAF14879 to AAF1537 represents ESTS from Aspergillus or and specifically claimed in the present invention.
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727 CAGTGATTGCATGCAGGATCGCGCATTTC 699

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AAS93068/c
ID AAS93068 standard; cDNA; 1182
                                                                                                                                                                 AAS93068;
                                                           RESULT 15
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                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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DNA encoding novel human diagnostic protein #28563.
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53.6%; Pred. No. 0.00
1ve 0; Mismatches
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2000US-0649167.
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P-PSDB; ABG28572.
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es 112; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                        WO200175067-A2.
                                                                                                                                       Homo sapiens.
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23-AUG-2000;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. A&S64197-A&S6454 represent novel human amino acid sequences. A&S64197-A&S6454 represent novel human
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46.5%; Pred. No. 0.0026;
artive 0; Mismatches 233; Indels 3;
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                                                                                         DNA encoding novel human diagnostic protein #28872.
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23-AUG-2000; 2000US-0649167.
13-FEB-2002 (first entry)
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1382 GATGGTCGGGGACGTGACGGACTGGGAGTACGTCAAGATCCGAATGCTCAATGCAGGGCA 1441
                                                                         1442 IGTCATGCTCTGCTTCCCAGGCATTCTGGTCGGCTATGAGAATGTGGATGACGCCATTGA 1501
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                       259 GGATCGCGCA---TTTCGCCATGCCGCCAGACATTAATGCTGGATGAGCAACGCGCGAC 203
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Copyright (c) 1993 - 2003 Compugen Ltd
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Sequence 1, Appli
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APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REPERENCE: 0867/00905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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Pred. No. 0.031;
0; Mismatches 135; Indels
                   PCT-US93-07213-3
US-09-232-279-1
US-08-682-847-1
US-09-481-288-14
US-08-114-692A-3
US-08-723-306-10041-3
US-08-723-306-10041-3
US-08-723-468-1
US-08-469-1
US-08-469-1
US-08-469-1
US-08-469-802B-1
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; OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4
                                                                                                                                                                                                                                                                  US-08-267-803B-1
US-08-457-273B-41
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US-09-041-886-14
US-08-246-982A-5
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US-09-130-114-2/c
; Sequence 2, Application US/09130114
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Best Local Similarity 48.1%;
Matches 125; Conservative
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ORGANISM: Epstein Barr Virus
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3010
279
932
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30001
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NAME/KEY: misc_feature
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US-08-286-870A-7/c
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US-08-286-870A-7
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48.1%; Pred. No. 0.031;
tive 0; Mismatches 135; Indels
                                                                  APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Enkaryotic Cells Stably Expressing Genes TITLE OF INVENTION: Enkaryotic Cells Stably Expressing Genes TITLE OF INVENTION: From Multiple Transfected Episomes FILE REPERENCE: 0867/10903051
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILLE DATE: 1998-08-06
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.0%; Score 43; DB 4; Length 477;
llarity 47.9%; Pred. No. 0.028;
Conservative 0; Mismatches 135; Indels
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Partent No. 6280938
Partent No. 6280938
Partent INFORMATION:
APPLICANT: Ranum et al.
TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/056,170
EARLIER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Horlick, Robert A.
                                                                                                                                                                                                                                                                                                                                         Query Match 1.1
Best Local Similarity 48.1
Matches 125; Conservative
                                                   APPLICANT: Damaj, Bassam B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-09-135-994-1
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124; Conserv
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US-09-130-114-2
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LENGTH: 477
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Matches 12
Patent No.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CUSHMAN DARBY & CUSHMAN ADDRESSEE: Intellectual Property Group of ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP STREET: 1100 New York Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.08
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ELY, S
APPLICANT: TAILOR, RH
APPLICANT: TIPPETT, JM
APPLICANT: BLENK, RG
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08286870A Patent No. 6063605 GENERAL INFORMATION:
                                                                                                                                                                                                         3597 CCTTCCGGCGAAAAGCGGC 3615
                                                                                                                                                                                                                                   CCCTGACGTCATCCGCGGC 58
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TELEFAX: (202) 822-0944
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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EDNESS: double
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20005-3918
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MOLECULE TYPE:
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5273901-6
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                                                                          TGTTATCGGGGGGGAACTGGAAGCAGGTCTTGAAAGCGTTGATTTCGTGTCGGTTCACCG 2818
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;Patent No. 5273901
; APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF,MICHAEL D.;
;AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
;TILE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
;SPOROZOTTE 21.5 KB ANTIGEN, AC-6B
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/581,693
; FILING DATE: 12-SEP-1990
; PRIOR APPLICATION NUMBER: 215,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 533;
                                                                                                                                                                                                                                                                                                APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON, SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF, MICHAEL D.; AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D. TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH SELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41.2; DB 6; Length 5 Pred. No. 0.095; 0; Mismatches 98; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,432
FILING DATE: 08-NOV-1993
PRIOR APPLICATION NUMBER: 581,693
FILING DATE: 12-SEP-1990
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1989
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
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FILING DATE: 05-JUL-1984
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Best Local Similarity, 52.9
Matches 111; Conservative
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;Patent No. 5482709
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3457 GITCIGICCAICCIGCCIGITCIGGGICIGIGGAIGCIGCCGGICGCCGIGAIGIIGCII 3516
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APPLICANT: Chung, Ming-Yi
APPLICANT: Zoghbi, Huda Yi
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
                                                                                                                                                                                                      Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.: 119 No. 5741645th Fourth Street, Suite 203
Minneapolis
                                                                                                                                                                                                                                                  Indels
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TITLE OF INVENTION: Type 1 and Method for Diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                0; Mismatches 106;
                                                                                                                                                                                                    Score 40.4; DB 6;
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3517 GCGCAGGATATTCCGTTCTTCCGTCGCCTT 3546
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FILING DATE: '06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
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FILING DATE: 05-JUL-1988
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 612-305-1217
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REGISTRATION NUMBER: 33, 
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                  Conservative
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 104; Conserva
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GENERAL INFORMATION:
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ZIP: 55401
                                                                                                                                   LENGTH: 543
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3443 TCATGCTGGGCGCGTTCTGTCCATCCTGCCTGTTCTGGGTCTGTGGATGCTGCCGGTCG 3502
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APPLICANT: Chung, Ming-Yi
APPLICANT: Zoghbi, Huda Yi
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
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ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
                                                                                   Score 40; DB 1; Length 234;
Pred. No. 0.13;
0; Mismatches 110; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
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REGISTRATION NUMBER: 36,602
REFERENCE/POCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
                                                                     1.0%;
cal Similarity 49.1%;
106; Conserved
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MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
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US-08-267-803B-3
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US-08-267-803B-3/c
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COUNTRY:
US-08-469-802B-3
                                                                                   Query Match
Best Local $
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3323 GCTCTGATGACGAACTGATGGATCTTTTGATCAAGCGTCTGCCCAATGTGGCTGCAGAAAG 3382

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1998477 CCATTGCCACCGCCTGGTTGACCCCCCGGGACCCGTTGCCGCTTGCCGTACAGA 1998418
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                                                                3383 IGCIGAACIGGIIGCGGGAAGCGGAICAIAAAIGGGIICGGAIICCGGCGGGGGGGTGCIGI 3442
                                                                                                                                                      3443 TCATGCTGGGCGGCGTTCTGTCCATCCTGCCTGTTCTGGGTCTGTGGATGCTGCCGGTCG 3502
                                                                                                        161 recreemecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecree
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                                                                                                                                APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILLE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2000/00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEC ID NOS: 2
SOFTWARE: PRECENTION VET. 2.1
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                                                                                                                                                                                                                                                                               ch 1.0%; Score 39.6; DE Similarity 52.4%; Pred. No. 25; 87; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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LENGTH: 4403765
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US-09-103-840A-1/c
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APPLICANT:
APPLICANT:
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Best Local
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                                                               Length 298;
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                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A FILING DATE: 09-JUN-1997 CLASSIFICATION: 435
                                                         Score 39.4; DB 2;
Pred. No. 0.22;
0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39.4; DB 3;
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
WUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PADSL, PALEA L.
REGISTRATION NUMBER: 31,284
REFERENCE/POCKET NUMBER: RPMS 101 CONTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/08871355A Patent No. 6015669 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                             1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8995
INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%;
    virulence gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 298 base pairs
nucleic acid
EDNESS: double
                                                                                                  67; Conservative
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                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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ZIP: 30309-3450
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  ; ORGANISM:
US-08-637-759B-21
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Best Local Simi
Matches 67;
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                                                                                                                                                                              Length 4411529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03.MAY 1996
                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                            Score 39.6; I
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING LHARE:

CLASSIFICATION 435

PRIOR APPLICATION ATA:

APPLICATION NUMBER: PCT/GB95/02875

FILING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: RPMS 101

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 873-8794

TELEPHONE: (404) 873-8795

INFORMATION FOR SEO ID NO: 21:

SEQUENCE CHARACTERISTICS:

TOWATH: 298 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                            ; TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
COTHEN INFORMATION: H37Rv
US-09-103-840A-1
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COMPUTER: IBM PC compatible
OPERATING, SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                              1.0%;
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nucleic acid
EDNESS: double
                 SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                       Matches 87; Conservative
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ZIP: 30309-3450
COMPUTER READABLE FORM:
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                            Query Match
Best Local Similarity
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STATE: Georgia
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                                                         LENGTH: 4411529
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0.9%;
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Best Local Similarity 48.2%;
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Matches 95; Conserv
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GENERAL INFORMATION:
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SEQ ID NO 36
LENGTH: 1794
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                                           61 GATGCGGCGTCTGTTGACCGACATGATGCTGGTGGCACGTGCCATTGCGACGG 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Partial sequence of Salmonella typhimurium ORGANISM: virulence gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                    Sequence 21, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/201,94'S FILING DATE: CLASSIFICATION: PRIOR APPLICATION APPLICATION APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8794
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                    Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 298 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                     Georgia
                                                                                                                                                                                                                                                                                                                                                            CITY: Atlanta
STATE: Georgia
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ORIGINAL SOURCE:
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Sequence 3, Application US/09253691 Patent No. 6124100

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3337 CTGATGGATCTTTTGATCAAGCGTCTGCCAATGTGGCTGCAGAAAGTGCTGAACTGGTTG 3396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dong Kyu JIN
TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
FILE REFERENCE: 1942/36
CURRENT APPLICATION NUMBER: US/09/253,691
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: KR 98-6,278
EARLIER FILING DATE: 1996-02-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: WordPerfect 6.1/Windows
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3457 GITCIGICCATCCIGCCIGITCIGGGICTGIGGAIGCIGCCGGICGCCGIGAIGTIGCIT
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Pred. No. 0.38;
0; Mismatches 117; Indels
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APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Harvey F.
TTTLE OF INVENTION: Fatry Acid Transport Proteins
FILE REFERENCE: WH197-21p3ME
CURRENT APPLICATION NUMBER: US/09/232,191
CURRENT FILING DATE: 1999-01-14
EARLIER FILING DATE: 1998-01-15
EARLIER PELICATION NUMBER: 60/03,491
EARLIER PPLICATION NUMBER: 60/03,491
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
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Pred. No. 0.95;
0; Mismatches 94;
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US-09-232-191-36
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Patent No. 6284487
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence 126, App	Sequence 1, Appl	Sequence 1, Appl	Sequence 27,	Sequence 491,	Sequence 393,	Sequence 261,	Sequence 158,	Sequence 718,	Sequence 26, App.	Sequence 27, App.	Sequence 28, A			85,	Sequence 1748	Sequence 2512, Ap	Sequence 103, 7	Segmence 1 Appl
	ID	US-09-738-626-126	US-09-738-626-1	US-09-802-208B-1	US-09-789-561-27	US-09-822-846-491	US-09-822-849A-393	US-09-822-849A-261	US-09-833-790-158	US-09-974-300-718	US-10-152-040-26	US-10-152-040-27	US-10-152-040-28	US-09-939-964-1	US-09-976-059-1	US-09-981-353-85	US-09-880-107-1748	US-09-738-626-2512	US-09-894-844-103	115-09-738-626-1
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æ	Query Match	5.2	5.2	2.6	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
	Score	213.6	213.6	105	42	41.6	41.4	41.4	41	40.4	40.4	40.4	40.4	40.4	40.2	40	40	39.6	39.6	39.6
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US-10-123-155-60	0 US-09-943-671-36				US-10-184-634-202	US-10-085-519-1	9 US-10-108-605-92		US-09-975-719-168				0 US-09-960-352-1970	10 US-09-894-882-8	9 US-09-946-807-1		10 US-09-795-686-1	_	-	US-10-127-391	US-09-764-891-8		ns	US-09-919	US-09-919-		ALIGNMENTS	
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                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PAPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR PELICATION NUMBER: JP 00/28098
PRIOR FILING DATE: 2000-08-03
NUMBER OF ESQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Corynebacterium glutamicum
US-09-738-626-126
Application US/09738626
o. US20020197605A1
                                                                    APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                             HAYASHI, MIKIRO
                                                                                                                                                                          OCHIAI, KEIKO
YOKOI, HARUHIKO
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APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
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Sequence 126, Appli-
Publication No. US2
GENERAL INFORMATION
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628 TCGGTGTAGGTAACTTTTTTCGAGCCCATGAGGCGTTCTACGTCGAGCAGATTCTTGAAC 687

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TAAAGGCCGACCTCAAGAACCCGGAAAAGCCGTCT-----
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APPLICANT: IXEDA, MASATO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES.
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PELING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum
                                                                                                                             ; Sequence 1, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
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APPLICANT: MIZOGUGHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
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SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
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Best Local Similarity
Matches 617; Conserv
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113 TCGGTGTTGGGGGATTCCATCGCGTCACCAAGCGATGTGACTCAATGAATTGATGAATG 172
                                                                                                                                                           GCAAGAGCACGGTGCGCGTCATGGGCGCGCTGCTTATCTGCTTGCCCCGGCCGATC 867
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Pred. No. 1.1e-54;
); Mismatches 609;
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CGGCAGTAAAGGCCGACCTCAAGAACCCGGAAAAGCCGTCTACCGTTTTCGGTTACGTGG 1041
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Best Local Similarity 46.8
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                                              GTTACGTGGTCGAGGCCCTGCGTCGTTGGGATGCCGGTGGTAAGGCATTTACGGTCA
                                                                                                           TGTCCTGTGATAACCTGCGTCATAACGGCAATGTCGCCCGCAAGGCCTTCCTCGGCTATG
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APPLICANT: Kane, Patrick
TITLE OF INVENTION: Arabitol or Ribitol As Por FILE REFERENCE: UGA-855R
CURRENT APPLICATION NUMBER: US/09/802,208B
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09802208B Publication No. US20300041352A1 GENERAL INFORMATION: APPLICANT: Parrott, Wayne
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US-09-802-208B-1
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TYPE: DNA
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                                                                                                                                                TITLE OF INVENTION: POLYUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS FILE REFERENCE: GIN 6400 CURRENT APPLICATION NUMBER: US/09/822,846 CURRENT FILING DATE: 2001-03-29 PRIOR APPLICATION NUMBER: 60/195,605 PRIOR FILING DATE: 2000-04-06 NUMBER OF SQ. ID NOS: 629 SOFTWARDEN PARTING APPLICATION PRIOR PRI
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Pred. No. 0.037;
); Mismatches 114;
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                                                                                       Resnick, Richard J.
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SEQ ID NO 393
                                                               Howes, Steven H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 491
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Matches 121; Conservative
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APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
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Clark, Hilary
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ORGANISM: Homo sapiens
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US-09-822-849A-393
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                                                                   1639 ACCAGACGCTCCGGATTGCTAGCGATGGCTGTTCCAAGGTTCAGGTGTTCTGGACGGAAA 1698
                                                                                                       1448 TCGATTTGCCAACCTACCGTGATGTTGTACTCAAGCGTTTTACCAATCCACATATTCAGG 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        647 GGTGCTCATGGTGGAGCTGTTCATGCGGGAGGAGCAAGAAAGCAGCAGCAGCTGCTGGAAAC 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1337 CCAGTTTGCGGATGGCCGTCCGCCGTTGA 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGATGGAGAGGAGCGGCAGAAGGACGA 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE TREAMENT APPLICATION NUMBER: US/09/789,561
CURRENT APPLICATION NUMBER: US/02/22
PRIOR APPLICATION NUMBER: PCT/USO0/24008
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 1999-09-03
PRIOR PLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER: OF SEQ ID NOS: 194
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42;
Pred. No. (
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/09789561
Patent No. US20020064818A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
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Steininger II, Robert
Bowman, Michael R.
Spaulding, Vikki
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Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.0
Best Local Similarity 50.0
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wong, Gordon G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-789-561-27
                                                                                                                                                                                                  1699 CCGTGCG 1705
                                                                                                                                                                                                                                                           1568 CACTGCG 1574
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APPLICANT:
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Length 2614;

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APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41.4; DB 10;
Pred. No. 0.034;
); Mismatches 121;
Sequence 393, Application US/09822849A Patent No. US20020045170A1
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/195,582 PRIOR FILING DATE: 2000-04-06
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Howes, Steven H.
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Matches 114; Conservative
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1150 ATGCGAAGGCGCGCGATCCGGAGTTGGCGAAGTGGATTGAGGAAAACGCGACCTTCCCGA 1209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 TCACCCACACGGTGCCCATCTACGAGGCTACGCCCTCCCCCACGCCATCCTGCGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                847 ATCTGCTTGCCCCGGCCGATCCGGAAGCCGTGCTGAAGCATCTTGTTGATCCGGCCATCC
              TITLE OF INVENTION: AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT PAPLICATION NUMBER: 2001-04-11
NUMBER OF SEQ ID DATE: 2001-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Berka, Randy M.
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT PELICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 40.4; DB 10;
46.1%; Pred. No. 0.068;
tive 0; Mismatches 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105;
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0.028;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 718, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LCCATTON: (1)...(501)
; OTHER INFORMATION: n = A.T.C or
US-09-833-790-158
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Similarity 49.8%;
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Tongtong
                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                  SEQ ID NO 158
LENGTH: 501
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                            FEATURE
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                                                                                                       GCGCGTCATGGGCGCGCTGCTATCTGCTTGCCCCGGCCGATCCGGAAGCCGTGCT
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APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
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Pred. No. 0.034;
0; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 261, Application US/09822849A Patent No. US20020045170A1 GENERAL INFORMATION: APPLICANT: Wong, Gordon G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-833-790-158
; Sequence 158, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fechtel, Kim
Agostino, Michael J.
Howes, Steven H.
Resnick, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.0%;
Best Local Similarity 48.5%;
Matches 114; Conservative (
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-822-849A-261
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-822-849A-261
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TYPE: DNA

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Length 1432;

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APPLICANT: VAN DER WERE, SYLVIE
APPLICANT: VIGNUZZI, MARCO
APPLICANT: VIGNUZZI, MARCO
APPLICANT: GERBAUD, SYLVIE
TITLE OF INVENTION: GENOMES USEFUL FOR THE PRODUCTION OF HETEROLOGOUS
TITLE OF INVENTION: PROTICINS
FILE REFERENCE: 03495,0229-00000
CURRENT APPLICATION NUMBER: US/10/152,040
EURRENT FILING DATE: 2002-06-27
PRIOR FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VIGNOZI, MARCO SINTE APPLICANT: VIGNOZI, MARCO APPLICANT: VIGNOZI, MARCO APPLICANT: GERBAUD, SYLVIE
TITLE OF INVENTION: REPLICONS DERIVED FROM POSITIVE STRAND RNA VIRUS TITLE OF INVENTION: GENOMES USEFUL FOR THE PRODUCTION OF HETEROLOGOUS FILE REFERENCE: 03495.0229-00000
CURRENT APPLICATION NUMBER: US/10/152,040
PRIOR FILING DATE: 2002-06-27
PRIOR FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: plasmid pM(DELTA)FM
US-10-152-040-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: plasmid pM(DELTA)BB-GFP-ICMVNP US-10-152-040-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4872 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCGTTTT 4831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCGGTTTT 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40.4; DB Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/10152040 Publication No. US20030077251A1
                                                                                                                                   Sequence 27, Application US/10152040 Publication No. US20030077251A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.0%;
Best Local Similarity 97.6%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ESCRIOU, NICOLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.09
Best Local Similarity 97.69
Matches 41; Conservative
                                                                                                                                                                                                                 APPLICANT: ESCRIOU, NICOLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 28 SOFTWARE: Patentin Ver. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patent
SEQ ID NO 28
LENGTH: 10417
                                                                                RESULT 11
US-10-152-040-27/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                      TGGAAGACCAGTTTGCGGATGG---CCGTCCGCCGTTGAAAAAGCCGG-----CGTGC 1380
                                                                                                                                                                                                                                                                                                                                                                                AGATGGTCGGGGACGTGACGGACTGGGAGTACGTCAAGATCCGAATGCTCAATGCAGGGC 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1441 ATGTCATGCTCTGCTTCCCAGGCATTCTGGTCGGCTATGAGAATGTGGATGAGACGCCATTG 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGACAGCGAACTCCTTGGCAATCTGAAGAACTATCTCAACAAGGATGTCATCCCGACCC 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1561 TGAAGGCGCCTTCAGGCATGACGCTCGAAGGCTATCGGGACAGCGTCATCAGCCGTTTCT 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1621 CCAACAAĠGCGATGTCGGACCAGACGCTCCGGATTGCTAGCGATGGCTGTTCCAAGGTTC 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1037 AAAACCCGTTTATCCGTCACAAGCTGATGTTTTCCTTAAATTCCTTTGCAAAATTCA 1096
                                                     1210 ACGGAATGGTTGATCGCATCACCCCGACCGTTTCGGCGGAAATCGCCAAGAAGCTCAACG 1269
                                                                                                                                                               CGGCCAGTGGGCTGGATGACGACCTGCCGCTGGTGGCCGAGGATTTCCATCAGTGGGTGC 1329
                                                                                                                                                                                                680 AGGCGCCGCTATCACGATTCCTTGATGGTGAAGGCGGAGCCGTATCATTTGTTCGTGA 739
                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTTGTCCAGGATGTGACGCCGTACAGGATAAGAAAAGTGAGAATTTTAAAACGCGCCC 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560 ACGCGTGGGCGCTTGAACAAGGGTTCATCGATTGGCTTGAAGAGGCAAACGTGTTCTGCA 619
                                                                                                       740 TTGAAGGCCCGAAATGGCTTCGAGACGAGCTTCCGCTTCATGAGGCCGGTCTGAATGTCG 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGA - - - CGAGCTTATCGGCTCATTTGTGAAAGAGCTGATCCAGCGGGAGGTGCTCGAGA
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APPLICANT: ESCRIOU, NICOLAS

APPLICANT: ESCRIOU, NICOLAS

APPLICANT: SCRIOU, NICOLAS

APPLICANT: GERBADD, SYLVIE

APPLICANT: GERBADD, SYLVIE

APPLICANT: GERBADD, SYLVIE

APPLICANT: GERBADD, SYLVIE

TITLE OF INVENTION: REDILCONS DERIVED FROM POSITIVE STRAND RNA VIRUS

TITLE OF INVENTION: PROTEINS

FILE REFERENCE: 03495.0229-00000

CURRENT APPLICATION NUMBER: US/10/152,040

CURRENT FILING DATE: 2002-06-27

PRIOR FILING DATE: 2001-05-23

PRIOR FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCGGTTTT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/10152040 Publication No. US20030077251A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 8017
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US-10-152-040-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-152-040-26/c
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Length 10417;

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NAME/KEY: misc_feature
LOCATION: (13617). (12802)
OTHER INFORMATION: ORF 9; negative strandedness
NAME/KEY: misc_feature
LOCATION: (15203). (13614)
OTHER INFORMATION: ORF 10; negative strandedness
NAME/KEY: misc_feature
LOCATION: (15591). (15863)
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INFORMATION: ORF 21; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           positive strandedness
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                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (9464)..(8130)
OTHER INFORMATION: ORF 6; negative strandedness
NAME/KEY: misc_feature
LOCATION: (9691)..(10761)
OTHER INFORMATION: ORF 7; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (12751)..(10829)
OTHER INFORMATION: ORF 8; negative strandedness
                               ORF 1; positive strandedness
                                                                                                                                                                                                                             ION: (4038)..(5048)
INFORMATION: ORF 3; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                              ION: (7703)..(6693)
INFORMATION: ORF 5; negative strandedness
                                                                                                          positive strandedness
                                                                                                                                                                              positive strandedness
                                                                                                                                                                                                                                                                                                        ION: (6665)..(5814)
INFORMATION: ORF 4; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: (65800)
OTHER INFORMATION: ORF 14;
NAME/KEY: misc_feature
LICCATION: (65826)..(66570)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCHER-INFORMATION: (71964)
OTHER-INFORMATION: ORF 20;
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (75535)..(76464)
OTHER INFORMATION: ORF 23;
NAME/KEY: misc_feature
LOCATION: (78110)..(76449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (15591)..(15863)
THER INFORMATION: ORF 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (15880). (19035)
THER INFORMATION: ORF 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (19032)..(39713)
OTHER INFORMATION: ORF 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ION: (66546)..(67370)
INFORMATION: ORF 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (67384)..(70059)
OTHER INFORMATION: ORF 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ION: (70099)..(70662)
INFORMATION: ORF 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ION: (70659)..(71906)
INFORMATION: ORF 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (75424)..(74213)
OTHER INFORMATION: ORF 22;
                                                                                                                               NAME/KEY: misc_feature
LOCATION: (4038)..(5048)
OTHER INFORMATION: ORF 3;
                                                    NAME/KEY: misc_feature
LOCATION: (3118)..(4032)
OTHER INFORMATION: ORF 2;
                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (6665)..(5814
                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (4038)..(5048
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LOCATION: (7703)..(6693
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LOCATION: (19032)..(397
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LOCATION: (39713)..(656
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LOCATION: (70099)..(706
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LOCATION: (15880). (190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (66546)..(673
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LOCATION: (70659)..(719
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LOCATION: (75535)..(764
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                                                                                                                                                                                                                                                                                                                                                                                                              OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185984 ATGACGTGGCGGGGGCGAAACCACCGACATAGAGCATCACTCGCTTGCCCTGGAGGCGC 485925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485924 GGCCAGTACTTGTCGATCACGGCGTCGACCAGCGGCCGGTACTTGGCGATGACCCTCTCG 485865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85864 GCCGGTTCTTCGATCGTCGGGCCGAAATGCCTGGTATCTTGCGCAGAGAGGCTTCGATC 485805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2785 GTCTTGAAAGCGTTGATTTCGTGTCGGTTCACCGGCCCGTCGATCTTCGCCAGCTTCGCG 2844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2845 CACAGGCCAACAAGGCCGATGGCGTAAAGCTGATCTCGTTTGCCCAGGGCCGCAGCAATC 2904
                                                                                                                                    Sequence 1, Application US/0993964

Sequence 1, Application US/0993964

Publication No. US20030054522A1

GENERAL INFORMATION:
APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARPO068
CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001.08-27
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2725 CGGGCGCGATCGAACAGCATGCCGACTTCCTTGGTGTTATCGGGGGGGAACTGGAAGCAG
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Patent No. US20020164747A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Farnet, Chris
APPLICANT: Sazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
FILE REPERENCE: 3019-PCT
CURRENT PILING DATE: 2001-10-15
NUMBER OF SEO ID NOS: 34
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 40.4; DB 9; Length 536165;
llarity 47.3%; Pred. No. 0.84;
Conservative 0; Mismatches 136; Indels 0;
7272 AAGCTIGCATGCCTGCAGTCGACTCTAGAGGATCCCGTTTT 7231
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SOFTWARE: Patentin Ver.
SEQ ID NO 1
LENGTH: 536165
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Matches 122; Conserv
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; ORGANISM: Rhizobium
US-09-939-964-1
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LENGTH: 88421
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; OTHER INFORMATION: a, t, c, US-09-981-353-85

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37124 GAGCTGGCGCTCGCGCAGGCTCTCCGGGTCACCGGCCGCCCCAGCAACTCCTCCTGCCA 37065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       positive strandedness; N-terminus only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 40.2; DB 9; Length 88421; 50.8%; Pred. No. 0.45; trive 0; Mismatches 93; Indels 0;
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OTHER INFORMATION: Incyte ID No. US20020160382A1 1102315.3
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APPLICANT: Lasek, Amy W.
APPLICANT: Lones, David A.
TITLE OF INVENTOR: GENES EXPRESSED IN COLON CANCER FILE REFERENCE: PA-0038 US
ORF 24; negative strandedness
                                                                  negative strandedness
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CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGram
SEQ ID NO 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 85, Application US/09981353 Patent No. US20020160382A1
                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (85556)..(86845)
OTHER INFORMATION: ORF 31; px
LOCATION: (87277
                    NAME/KEY: misc_feature
LOCATION: (79864)..(78107)
OTHER INFORMATION: ORF 25; nc
NAME/KEY: misc_feature
LOCATION: (81624)..(79861)
OTHER INFORMATION: ORF 26; nc
NAME/KEY: misc_feature
LOCATION: (81909)..(81682)
OTHER INFORMATION: ORF 27; nc
                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (82346)..(8206)
OTHER INFORMATION: OFF 28: 06
NAME/KEY: misc_feature
LOCATION: (82587)..(84446)
OTHER INFORMATION: OFF 29: pc
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OTHER INFORMATION: ORF 32;
NAME/KEY: misc_feature
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OTHER INFORMATION: ORF 30;
NAME/KEY: misc_feature
LOCATION: (85556)..(86845)
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Best Local Similarity 50.8
Matches 96; Conservative
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LOCATION: 2713, 2719, 3094
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US-09-981-353-85/C
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2628 GAACAGTGCCGTCATGAGGTTCTCAAGCGGCGCGTATTATCGGCATAGGCCTTGCCCAT 2687
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                                                                                                             773 GCACAGGTGGTAGATGAAGGACCCCAGGGCCTCCTTGTCACTGACATGCTCCGTGACCAC 714
                                                                                                                                                                       713 CATCTCCTCGATGATGTACGTCTGCGGCAGGTACGTCCCCCTCTTCACGTTCATGAG 654
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   Length 3115;
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Pred. No. 0.13;
0; Mismatches 150;
 1.0%;
                                      Matches 130; Conservative
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Search completed: May 18, 2003, 21:32:28 Job time : 3984 secs

AW671891 LG1_352_G BI191448 lle03fs.r BI191768 lle03fs.r BH143537 TDCEB13TH AQ500091 V34C6 mTn BG608411 296895 MA AZ933800 BJ_BB0000 AL108460 Drosophil

AL539916 AL53993

BE733079 60156958 A257883 28a07 Sho B0672858 AGENCOURT BN549784 AGENCOURT B1600315 603250632 BGB1826 60279895 BGB1826 60279895 BA6470953 60271926 BC74237 602711926 BC74237 602711926 BC75926 AGENCOURT BM65009 AGENCOURT BM65009 AGENCOURT BM563059 AGENCOURT BM653013 AGENCOURT BM653013 AGENCOURT BM653013 AGENCOURT BM653013 AGENCOURT BM653013 AGENCOURT BM656060 AGENCOURT BM656060 AGENCOURT BM676605 AGENCOURT BM676139 AGENCOUR

Run on:

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AG-ND-144F15.TR ND-TAM Anopheles gambiae genomic clone AG-ND-144F15 BH395246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
Other_GSSs. AG-ND-14fF15.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library (Second): CHOMINS and Sequenced by The Institute for Genomic Research
[TIGR]. The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                           CNS017SY
AL539916
BE733079
                                                                                   AZ578838
BQ672858
BQ641340
BM549784
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BG818263
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BM562009
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BQ950903
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BG756596
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BB643958
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BI856423
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BQ231485
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AZ139030 SP_0178_B
BE641454 Cri2_3_F0
AL15645 Anopheles
AA965891 08906a1.r
AZ049105 GSSBru050
                                                                  (without alignments)
12382.837 Million cell updates/sec
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                                                                                                             1 aagcttgcatgcctgcaggt......tccgggcgggcgggcttgaagctt 4115
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                                                         May 18, 2003, 21:32:35; Search time 5382 Seconds
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        5.1.6
Compugen Ltd
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        GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                     summaries
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BE641454
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                                         nucleic search, using sw model
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A1929012 au64a11.y BQ231485 AGENCOURT BG764520 602736565

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to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&W Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGGAAGGCGCCTACAACATCAACGAGACGACCGTGCGTTCGATCTGGAGAATGCGGCA
                                                                                                                                                                                                                                                                                                                                                                                GATGGCCGTCCGCCGCTTGAAAAAGCCGGCGTGCAGATGGTCGGGGACGTGACGGACTGG
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                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                        Score 180.8; DB 17; Leus----
Pred. No. 2e-36;
                                                                                                                                                                  /clone="AG-ND-144F15"
/clone_lib="ND-TAM"
/note='Vector: pECBAC1; Site_1: HindIII"
162 c 156 g 273 t
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                                                                                                                         /organism="Anopheles gambiae'
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/db_xref="taxon:7165"
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ilarity 55.4%;
Conservative (
                                                     partial digest.
Seg primer: M13 Rev
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AZ139030 SP_0178_BZ_F03_T7A Strongylocentrotus purpuratus, purple sea urchin sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate-178 Col=6 RoweL, DNA sequence.

LOCUS

AZ139030/c

RESULT 2

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urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
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                                                                                                                                                                                                       Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. ar Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1284 GATGACGACCTGCCGCTGGTGGCCGAGGATTTCCATCAGTGGGTGCTGGAAGACCAGTTT
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Echinoidea; Euechinoidea; Echinacea; Echinoida;
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Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
20402566
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/db_xref="taxon:7668"
/clone="Plate=178 Col=6 Row=L"
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Pred. No. 1e-29;
); Mismatches 266;
                                                                                                                                                           Strongylocentrotidae; Strongylocentrotus
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Division of Biology 156-29
California Institute of Technology
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Location/Qualifiers
1. .761
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                                                 Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
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Plate: 178 row: L column:
Seq primer: T7
Class: BAC ends
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Fax: (626) 793-3047
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Best Local Similarity 54.2
Matches 315; Conservative
AZ139030.1
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1116 AACGGCAATGTCGCCCCGCAAGGCCTTCCTCGGCTATGCGAAGGCGCGCGATCCGGAGTTG 1175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS01QW5 Anopheles gambiae GSS SP6 end of clone 31M20 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                               CCCGTTTGTCACCGAACCCTCATGCATGGGGTCTTTGAGGAACAGTTCAGCGAAGGGCCC 818
                                                                                                                                                                                                        GGCTACTACTACCACGAAAAACACCCACGAGCTGCAGGCCAACCATTCCGACATCCAGCAC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cèdex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                       280 TTCGCCAACGTCGTCGCCAGCATCAACTCGTTCCTCTTCGCCCCGGACGACGCGAGGCC 339
                                                                                                                                                                                                                                                                                                                                       520 AAGGGCCACGCGAAGGCCTGAAGGCCTTCACCGTCATGTCCTGCGACAACATGCAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGCTGAAGCATCTTGTTGATCCGGCCATCCGCATCGTTTCCATGACGATCACGGAAGGC
                                                                                                                                                                     GGCTACAACATCAACGAGACGACCGGTGCGTTCGATCTGGAGAATGCGGCAGTAAAGGCC
                                                                                                                                                                                                                                                                             460 GACCTGGCCAACGAGAAAGGCCCCGTCAGCACTTTGGCTTCCTCTACGCCGCGCGTGGCC
                       ACGGTGCGCGTCATGGGCGCGCTGCGTGACTATCTGCTTGCCCCGGCCGATCCGGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roth, C.W., Brey, D.T., Ke, Z., Collins, F.H. and Weissenbach, J. Direct Submission
Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eb : www.genoscope.cns.fr) (bases 1 to 799)
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AUTHORS
TITLE
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JOURNAL
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGAGTACGTCAAGATCCGAATGCTCAATGCAGGGCATGTCATGCTCTGCTTCCCAGGC 1463
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chatterjee.A., San Miguel, P., Stout, S.C., Banks, J. and Roux, S.J.
Expressed sequence tags of .CDNA clones from a C. richardii library
Unpublished (2000)
Contact: Roux SJ
Section of Molecular Cell and Developmental Biology
University of Texas
Biology Building, Room 16, Austin, TX 78712, USA
Tel: 512 471 4238
Fex: 512 232 3402
576 GTCCAGGCTCCCCCCTATGACATCGACGGGATCAAGCCTGGGATCGTGCATTTCGGTGTA 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ta; Embryophyta; Tracheophyta; Pteridaceae; Ceratopteris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          756 GAATICAAGGCCCAGGACTGCCTGTAITCCCTGACCGAGACGCCTCCGTCCGGCAAGAGC 815
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                                                                                                                             1464 ATTCTGGTCGCCTATGAGAATGTGGATGACGCCATTGAAGA 1504
                                                                                                                                                  /organism="Ceratopteris richardii"
/cultivar="Brogn"
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Pred. No. 2e-27;
0; Mismatches 392;
                                                                                                                                                                                                                                                                                                                                                                                                            Streptophyta;
Filicales; Pte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: sroux@uts.cc.utexas.edu
Plate: Cri2_3 row: F column:
Seq primer: SP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  Ceratopteris richardii.
Ceratopteris richardii
Eukaryota, viridiplantae; St
Filicophyta; Filicopsida; Fi
1 (bases 1 to 840)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o8906al.rl Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone o8906al 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                          529 CCTTTATCGTCGCAGACCTGMAAAACCCGCACCAGCCGAAATCTGCGCCGGGTGTGGTC
                                                                                                                                                                                                                                                                                                                                           GTAGACGTGAGCTGGCGGACTGGATCCCACGTTACCTTCCCGTCAACGATGGTG
                                                                                                                                                                     GCCGATCCGGAAGCCGTGCTGAAGCATCTTGTTGATCCGGCCATCGCATCGTTTCCATG
                                                                                                                                                                                              GACGGGCTCGAGACCGTCCTGGCCGCGATGTGCGAACCGCAGGTGGCGATTGTGTCGCTG
                                                                                                                                                                                                                        ACGATCACGGAAGGCGGCTACAACATCAACGAGACGACGGTGCGTTCGATCTGGAGAAT
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                                                                                                                     DB 17; Length 799;
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                                                                             others
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Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eutotiales; Trichocomaceae; Emericella.
1 (bases 1 to 527)
                                                                            30
                                                                                                                  Score 131.8; DB 17;
Pred. No. 1.8e-23;
5; Mismatches 302;
/organism="Anopheles gambiae
                                                                             ψ,
      /strain="PEST"
/db_xref="taxon:7165"
/clone="31M20"
/clone_lib="NotreDame1"
/note="end: SP6"
a 245 c 206 g 167
                                                                             167
                                                                                                                  3.2%;
larity 51.6%;
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481 bp DNA linear GSS 01-SEP-2000 Ascrue GSS 01-SEP-2000 Abortus genomic library Brucella melitensis biovar Azottus genomic clone B4G18, DNA sequence.
Azot49105.1 GI:7273020
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/db.xref="taxon:162425"
/db.xref="taxon:162425"
/clone="08906al"
/clone="naspergillus nidulans 24hr asexual
/clone="laspergillus nidulans nidulans 24hr asexual
/clone="laspergillus nidulans nidulans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335
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                                                                                                                                  Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
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Pred. No. 3.9e-12;
); Mismatches 198;
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Prade, R. and Roe, B.
An Aspergillus nidulans EST Database
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 We anticipate the future release of
Genetics Stock Center
Seg primer: T3
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Location/Qualifiers
1 .527
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AW671891
AW671891.1
                                                                                                            Eukaryota;
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                                                                          sorghum.
Sorghum b
       sednence.
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                                                                                         ORGANISM
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KEYWORDS
SOURCE
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                                                                                                                                                                                                TITLE
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                                                                                                                                                            REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Sheared genomic library"
/note="Vector: pBluescript SK(-) (STRATAGENE); Genomic DNA
was mechanically sheared, blunt ended, and
size-fractionated by agarose gel electrophoresis.
Fragments between 1.5-3 Kb were recovered and ligated to
the EcoRV site of the pBluescript SK (-) vector."
136 c 130 g 105 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1079 GGCATTTACGGTCATGTCCTGTGATAACCTGCGTCATAACGGCAATGTCGCCCGCAAGGC 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1139 CTTCCTCGGCTATGCGAAGGCGCGCGATCCGGAGTTGGCGAAGTGGAATTGAGGAAAACGC 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1318 ATCAGTGGGTGCTGGAAGACÇAGTTTGCGGATGGCCGTCC-GCCGCTTGAAAAAGCCGGC 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1199 GACCTTCCCGAACGGAATGGTTGATCGCATCACCCCGACCGTTTCGGCGGAAATCGCCAA 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1377 GIGCAGAIGGICGGGACGIGACGGACIGGGAGIACGICAAGAICCGAAIGCICAAIGCA 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1259 GAAGCTCAACGCGGCCAGTG-GGCTGGATGACGACCTGCCGCTGGTGGCCGAGGATTTCC 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 GCCGTTTACCGTTCTTTCCTGTGATAATCTGCCTGCCAATGGCGAAACCTGCAAAACGT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 GATCGTGCAGTTTGCGGGATGCACGGACACAGATCTGGCGCCATTACATTGAANAAACGGT 169
                                                                                                                                                         abortus genome
Unpublished (1999)
Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                              Brucella
                                                                                                                                                                                                                                                 Av. Gral Paz entre Albarel·los y Constituyentes, INTI edificio 24 (2P(1650) San Martin, Prov. de BS AS. Argentina Tel: 54-11-4580-7255 ext 309 Fax: 54-11-4752-9639
                                                                                       1 (bases 1 to 481)
Sanchez,D.O., Zandomeni,R., Cravero,S., Rosetti,O., Grau,O. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 TGCCTTCCCGTCAACAATGGTCGATTGTACCGGCAACGACGATGAAGACGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 ATCCATCAGCAGGGACGCTGAAGTTCTGGATCAATGGCCAATCACCACCAGCCTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 GCAACCTTCGTGCAGGATGTAGCAGCTTTTGAATTGATGAAACTGCGCCTGCTCAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Brucella melitensis biovar Abortus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 481;
                                                                                                                                          Gene discovery through genomic sequencing survey of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86.6; DB 17;
Pred. No. 1.3e-11;
0; Mismatches 181;
                  Brucella melitensis biovar Abortus.
Brucella melitensis biovar Abortus
                                                                                                                                                                                                                                                                                                                    Email: dsanchez@iib.unsam.edu.ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:235"
/clone="B4G18"
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .481
                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="S-2308
                                                                       Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.1%;
Best Local Similarity 54.1%;
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                         Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       primer:
                                                                                                                                                                                                                                    San Martin)
                                                                                                                         Ugalde, R.
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                                   ORGANISM
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                                                                                     REFERENCE
                                                                                                          AUTHORS
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                                                                        bicolor
ta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Coloreae; Pacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGCGCGTCATGGGCGCGCTGCGTGACTATCTGCTTGCCCCGGCCGATCCGGAAGCCGTG 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    879 CTGAAGCATCTTGTTGATCCGGCCATCCGCTTTCCATGACGATCACGGAAGGCGGC 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              505 ATCGCCAAGATGGCTCACCGACACCTCACATGACTATCACAGAGAGGGGG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_l: XhOI; Site_2: Eco
; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACAACATCAACGAGACGACCGGTGCGTTCGATCTGGAGAATGCGGCAGTAAAGGCCGA 997
                                                                                                                             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 CCTACCTACGACCGTTCTAGCATCAAGCATGGTATCGTCCACGTTGGTGGTGTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 TGGGCTATCTGCGGTGTTGGCATGCAGTCCTTCGATGAGATGAGGGATGCCC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                             and Pratt, L.H.
                                                                                                                                                                                                                                                                                                                  Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 624;
                                                                                                                                                                                                An EST database from Sorghum: light-grown seedlings Unpublished (2000)
Contact: Cordonier-Pratt MM
Laboratory for form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 3e-11;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared by mass excision."
217 c 135 g 126 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: JEN REV
High quality sequence stop: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                           The University of Georgia, De
Plant Sciences Building, Rm.
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mmpratt@uga.edu
GI:7535792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%;
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Best Local Similarity 55.6%;
Matches 233; Conservative
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RESULT

AW671891 624 bp mRNA linear EST 19-JUL-2000 LG1_352_G02.b1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA

LOCUS DEFINITION 9

513

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Evarium sporotrichioides.

Eukaryotra: Fungi: Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryotra: Fungi: Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryotra: Fungi: Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.

E 1 (bases 1 to 519)

I (bases 1 to 519)

M. and Roe, B.

Analysis of a Fusarium sporotrichioides EST database

L (unpublished (2001)

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Departument of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Parrington oval, Norman, OK 73019, USA

Tel: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="vector: pBlueScript SK-; Site_1: EcoR1; Site_2: Xhol; 5' end of cDNA cloned into EcoR1 site of pBluescript i 3' end of cDNA cloned into XhoI site of pBluescript" i 16 c 116 g 100 t
                                                                                                                                                                                               EST 10-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCAGGTCCCATCCTACGACCGCAAGTCGCTCAAGGAGGCCATCGTTCACGTCGGAGTT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTGGGCGATTGTTGGTGTTGGCCTGACGGGCAGTGACCGTTCAAAGAAAAAAGCCGAG 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCGCGATTGGGCCATCTGCGGTATCGGCCTGCGTCCTAACGATGCTGCCATGCGGGAT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact Dr. Marian Beremand regarding clone availability Include is the best homolog from a blastx search of Genbank nr 04-09-01 455 5e-45 gi|805056|emb|CAA604 (x86790) N3810 [Saccharomyces
157 GGCGGTTTCCACAGAGCTCATCTGGCTGTCTATGTCGACAAGCTGCTCGAGAAGCATGGT
                                                                                                                                                                                               BI191768 120-JUL-
12e03fs.rl Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone 12e03fs 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTAACTTTTTCGAGCCCATGAGGCGTTCTACGTCGAGCAGATTCTTGAACACGCTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 519;
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Location/Qualifiers
1. 519
/organism="Fusarium sporotrichioides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80.4; DB 13;
Pred. No. 5.7e-10;
); Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Tri 10"
/db_xref="taxon:5514"
/clone="12e03fs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.0°
Best Local Similarity 50.9°
Matches 217; Conservative
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                                                          996 GACCTC 1001
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                                                                                                                                                        Fusarium sporotrichioides.

Fusarium sporotrichioides

Fusarium sporotrichioides

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreales; mitosporic Hypocreales; Fusarium.

E 1 (bases 1 to 519)

S Ren, O., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand

M. M. and Ree, B.

Analysis of a Fusarium sporotrichioides EST database

L Unpublished (2001)

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Departument of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Partington Oval, Norman, OK 73019, USA

Tel: 405 325 4912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA library"

Anote-"Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of CDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript
1 166 c 116 g 100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI191648 linear EST 10-JUL-2001 11603fs.rl Fusarium sporotrichioides Tri 10 overexpressed CDNA library Fusarium sporotrichioides CDNA clone lle03fs 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: broelou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
455 5e-45 gil805056|emb|CAA604 (X86790) N3810 [Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         576 GTCCAGGCTCCCCCTATGACATCGACGGGATCAAGCCTGGGATCGTGCATTTCGGTGTA
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Pred. No. 5.7e-10;
0; Mismatches 206;
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Location/Qualifiers
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BII91648.1 GI:14665327
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sl Similarity 50.9%;
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/tissue_type="Young leaves"
/dev_stage="12-14 weeks post harvest"
/lab_host="cool JMN09"
/note="Vector: paluescript SK(·); Site_1: EcoRI; Site_2:
/note="Vector: paluescript SK(·); Site_1: EcoRI digested
fragments of the genome of Lycopersicon esculentum ligated
into pBS (SK-). The fragments were cloned into the
methylation restrictive E.coli strain JMN09 with the
purpose of enriching the library for non-methylated DNA
fragments. This procedure may enrich the pool of cloned
fragments in JMN09 cells for sequences representing
expressed genes. Average insert size 1.27 kb."
                                                                                                                                                                                                                                                                                                                       BH143537 520 bp DNA linear GSS 16-AUG-2001
TDGEB13TH CTOG Lycopersicon esculentum genomic clone cTOG27C2, DNA
                                                                                                                                    GGCTACAACATCAACGAGGACGGTGCGTTCGATCTGGAGAATGCGGCAGTAAAGGCC 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
816 ACGGTGCGCGTCATGGGCGCGCTGCGTGATCTGCTTGCCCCCGGCCGATCCGGAAGCC 875
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van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Ronning,C. and
                                                                                     337 GCCGA---CGTTGTAGGCAGTATCACCTCCTTCATTTTCGCTCCCGACGACCGTGAGGCC
                                                                GTGCTGAAGCATCTTGTTGATCCGGCCATCCGTTTCCATGACGATCACGGAAGGC
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
"Email: http://www.genome.clemson.edu/orders/index.html
tomato demethylated genomic DNA
tomato demethylated genomic Std Error: 0.00
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ilarity 48.4%; Pred. No. 3.2e-09;
Conservative 0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomato Demethylated Genomic DNA Sequences Unpublished (2001)
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/organism="Lycopersicon
/cultivar="E6203"
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Class: shotgun.
                                                                                                                                                                                                     GACCTC 1001
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514 GATCTC 519
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556 bp DNA linear GSS 29-APR-1999 V34C6 mTn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae genomic 5', DNA sequence.
AQ500091.1 GI:4704913
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                                                                                                                                                                                                                                                                                                                                                                  846
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                                                                                                                        AGCAGATTCTTGAACACGCTCCGGACTGGGCGATTGTTGGTGTTGGCCTGACGGGCAGTG 732
                                                                                                                                                                                 ACTTGGCCATGACCGCCAGCGGGGACCTGAGTTGGGGCCATCGTGGGCGTTTCGCTGCGCA 183
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Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                               AGACGCCTCCGTCCGGCAAGAGCACGG-----TGCGCGTCATGGGCGCGCTGCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    847 ATCTGCTTGCCCCGGCCGATCCGGAAGCCGTGCTGAAGCATCTTGTTGATCCGGCCATCC
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                                  ACCGTTCAAAGAAAAAGCCGAGGAATTCAAGGCCCAGGACTGCCTGTATTCCCTGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4932"
/clone_lib="mTn-3xHA/lac2 Insertion Library"
/lab_host="E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene Disruption
Unpublished (1999)
Contract: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Fax: 203 432 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1027 TTTTCGGTTACGTGGTCGAGGCCCTGCGTCGTCG 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 CCATCGGCATCCTGGTGTACGGCCTGGCGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: GCCCTTCTTTCTTTGGAAGTAC Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           te of mTn-3xHA/lac2 insertion
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AZ933800
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                                                                                                                                                                                                                                                                                                                                        Matches
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AZ933800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.909004.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 17-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith, T.P.L., Casas, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    992 GGCCGACCTCAAGAACCCGGAAAAGCCGTCTACCGTTTTCGGTTACGTGGTCGAGGCCCT 1051
                                                                                                                                                                                                                                                                                                                                                                          ||| | | | | |||||||| || ||||| || |||| || ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 TAACGCTTATATCGTC---GGTTCCATTACTGCTTACATGTACGCTCCCGATGATCAAG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 AGCTGTTATTGAAAAGATGGCCAATCCAGACACACACTTGTTTCTTTGACGGTCACAGA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       812 GAGCACGGTGCGCGTCATGGGCGCGCTGCGTGACTATCTGCTTGCCCCGGCCGATCCGGA 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCCGTGCTGAAGCATCTTGTTGATCCGGCCATCCGCATCGTTTCCATGACGATCACGGA 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGCGCCTACAACATCAACGAGACGACCGGTGCGTTCGATCTGGAGAATGCGGCAGTAAA 991
genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mTn-3xHA/lac2 minitransposon containing lac2, URA3, and tet resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Design and use of two pooled tissue normalized cDNA libraries for Unpublished (2000)
CONTACT: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases I to 506)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                     1.7%; Score 69.4; DB 17; Length 556; 52.2%; Pred. No. 4.8e-07; tive 0; Mismatches 161; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296895 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BG608411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1052 GCGTCGTCGTTGGGATGCCGGTGGTAAGGCATTTACGGTCATG 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 GTTGTTGCGTTACAAGAGAGGTCTTACCCCATTCACTATTAGG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 1 row: A column: 22
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. 506
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/clone_lib="MARC 1PIG"
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                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                              Best Local
Matches 1
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VERSION
KEYWORDS
                                                                                                                                            SASE COUNT
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BG608411
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אנפיבים 188 bp DNA linear GSS 24-APR-2001 BJ_Ba0001c08f B. japonicum BAC library Bradyrhizobium japonicum penomic, DNA sequence.
                                                                                                                                                                                                                                                                                                                   1241 TICGGCGGAAATCGCCAAGAAGCTCAACGCGGCCAGTGGGCTGGATGACGACCTGCCGCT 1300
                                                                                                                                                                                                                                                                                                                                                                                                                           1301 GGTGGCCGAGGATTTCCATCAGTGGGTGCTGGAAGACCAGTTTGCGGATGGCCGTCCGCC 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1361 GCTTGAAAAAGCCGGCGTGCAGATGGTCGGGGACGTGACGGACTGGGAGTACGTCAAGAT 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1421 CCGAATGCTCAATGCAGGGCATGTCATGCTCTGCTTCCCAGGCATTCTGGTCGGCTATGA 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loh, J.T., Judd, A., Goicoechea
                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 TAGCTGCGAACCGTTTATCCAGTGGTGGTGGAAGATAACTTCATCGCTGGGCGTCCTGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 CTGGGAAGTCGCAGATGTACAATGGTGAATGATGTCCTGCCATGGGAAGAGATGAAACT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 GCGGATGCTTAATGGCAGCCACTCTTTTCTCGCTTATCTGGGTTACCTCTCAGGATTCGC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 788)
Commins. J. P., Wood, T. C., Stacey, M. G., Loh, J. T., Judd, A., Goicoechee, J. L., Stacey, G., Sadowsky, M. J. and Wing, R. A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                                                          61
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
118 c 138 g 120 t
                                                                                                                                                                                                                                                                                                                                                                       2 TGCACCGACAATACTGGTGGAAATCAGCCAGCATCTGGGGGGTGAATGATCCCTGCGCGAT
                                                                                                                                                                                                                                                                        Gaps
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271 c 258 g 131 t
                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                     Indels
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/clone_lib="B. japonicum BAC library"
/lab_host="E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bradyrhizobium japonicum"
/strain="USDA110"
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                                                                                                                                                                                                                                                                     0; Mismatches 138;
                                                                                                                                                                                                                    DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 CCATATCAGTGATTGCATGCAGGATCGCGCATTTC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                    Score 54.2; DB 1:
Pred. No. 0.0048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 11 (8), 1434-1440 (2001)
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Bradyrhizobiaceae; Bradyrhizobium.
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Location/Qualifiers
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Class: BAC ends
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BTBBSSBSBSSSSSTSSSBBTSKSBTSBSSBSTSSSASBSSSSSSBSSTSTTBSTSBBB 930
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                                                                                                         2498
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TITLE
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                              1602 AGGGCATCAGCGGTTTCTCCAACAAGGGGATGTCGAACACACAGACGGATTGCTAGC 1661
                                                    1422 CGAATGCTCAATGCAGGGCATGTCATGCTTCCCAGGCATTCTGGTCGGCTATGAG 1481
                                                                                                                      1482 AATGTGGATGACGCCATTGAAGACAGCGAACTCCTTGGCAATCTGAAGAACTATCTCAAC 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 TGCGGGCCACCCGGTCCTGTGCGCGTTTGCGCTCTGTCTCTGACATAGGTTTCTGGGCCA 2377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web: www.genoscope.coms.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2378 GCACGTCCGGATGATGTTCGCGGATCAGGGTGCGCCAGCGCACGCGGATTTCTGTGTGAG 2437
                                                                                                                                            61 ACCATCGCCGACACCATGCAGATCCGCATTC---GCGCGTCTCGCCGCGCGCGTGTTT 117
                                                                                                                                                                                                                118 GAAGAGGCGGGGGAAGGTGCCGGCGAGCACCGACCTTGCCGCCTATCGCGCC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                  178 TCGCTGCTCCAAGCGCTTCGCCAATCCGGCGCTGCATCGTCGCACCTGGCAGATCGCGATG 237
                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ceecrecreaceccaeccarrececerrecerrareresecratereses
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera: Endotherygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone="BACN37L08"
 Pred. No. 0.034;
0; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2%; Score 49.2; DB 17;
16.1%; Pred. No. 0.16;
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/plasmid="pBeloBAC11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                     1662 GATGCCTGTTCCAAGGTTCAG 1682
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 52.5%;
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137; Conservative
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Direct Submission
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pcMvSpORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville (Maryland 20850, USA Fax: (1) 301 610 8371 Email: http://tulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="CSODF031YM10"
/clone_11b="LTI_FL013_FBrn1"
/dc_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
                                                                                                                                                                                                                                                                                                                                                                       2618 GGGCGATACGGAACAGTGCCGTCATGAGGTTCTCAAGCGGCGCCGTATTATCGGCATAGG 2677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL539916 ALI_FL013_FBrn1 Homo sapiens CDNA clone CSODF031YM10 5
                                                                                                                         GATTGTTGCCGCTTTCGGCCCGGTCCCATGCTCCTGGCGGCAGGCCAAATGCCCCGTGAA 2557
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                                                                                                                                                             SSBSTTTSBSSTBSSYGSSSBTCTSKCSTBTSGSTBTSTBMSKBSSTSSTSBTSGSSBCG 810
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                                                                                                                                                                                                                                                                                                          809 GSCGSTSGSSCSSBCGKSTSSGSTSSGTTCGBCSSTGGCSCCCYCSCCCTCSTCGTSTCC 750
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Primates; Catarrhini; Hominidae; Homo.
2438 TTGCGCTGCGGGTGATGCCGAGAATACGATAGGCATCCGGCTCGTTTCCGCTGGCGGCGC
                                      STSSSSSSBBSTTTBBSBSSBTTTTBTRKSTSSSSTSBTTTBBBSSSSSSBS
                                                                                                                                                                                                                                             CGCGCTGCAGAAAATCGATTTCCTTCGGGTGAAGCTCGCGGCTGGGGCCGGCATCGGCCAC
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Mammalla; Eutheria; Primates; Catarrhini; Hon
1 (bases I to 861)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Ful. 1ength cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 0.28;
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    Qy
    821 GCGCGTCATGGGCGCGTGATCTGCTTGCCCCGGCCGATCCGGAAGCCGTGCT 880

    Db
    379 CTCCCCCGCCATCCTGGACCTGGCTGGCGGGACCTGACGATACCTCAT 438

    Qy
    881 GAAGCATCTTGATCCGGCCATCCGCATCGTTCCATGACGATCACGGAAGCGGCTA 940

    III
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    Qy
    941 CAACATCTCATGAGCGAGCTACAGCTTCACCACGGCGGCGAGTGTGGGGAATTCGTGCG

    Qy
    941 CAACATCAACGAGACGACCGGTGCGTTCGATCTGGAGAATGCGGCAGTAAAGGCCGACCT
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9 6y 6b

Search completed: May 19, 2003, 01:48:00 Job time : 5397 secs

Human secretory pr Human angiogenesis

PRÓ1273 prot PRO protein,

Human secreted pro Human testicular a

reproductive Orosophila melanog Propionibacterium Peptide #10729 enc Protein #8303 enco

Human brain expres Peptide #7474 enco Peptide #11100 enc Human peptide enco Propionibacterium Peptide #10959 enc

Human brain expres Arabidopsis thalia

Protein #8420 enco Human brain expres Human bone marrow Peptide #7571 enco Peptide #11378 enc Human cardiovascul Human secreted pro Human protein SEO

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Saito Y;

Score

Result Š.

Human peptide enco Human ovarian anti

Lactococcus lactis Herbicidally activ Peptide #10867 enc

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Word size :

Searched:

Database :

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D-sorbitol dehydrogenase; SLDH; L-sorbose production; NADP+ dependent; sorbitol; mannitol; arabitol; oxidation; 2-keto-L-gluconic acid; L-ascorbic acid biosynthesis; vitamin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gluconobacter oxydans D-sorbitol dehydrogenase (SLDH).
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ABG46062
AAU54359
ABB43453
ABB26421
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AAU59450
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AAM37341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB23172 standard; Protein; 485 AA.
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99JP-0224679.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2001 (first entry)
                                                                                                                                                                   Shibata T, Ichikawa C,
Zamashita M, Takata Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gluconobacter oxydans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-587530/55.
N-PSDB; AAA97430.
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06-AUG-1999;
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Gluconobacter subo
Gluconobacter subo
Gluconobacter subo
Human reductase-li
Human PRO1273 (UNQ
Human PRO1273 poly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gluconobacter subo
Gluconobacter oxyd
C glutamicum prote
Corynebacterium gl
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1615.664 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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/SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:
/SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:
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/SIDS2/gcgdata/geneseq/genesegp-emb1/AA1981.
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                                                                                                     8, 2003, 16:34:43; Search time 40 Seconds
            GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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AAG89872
AAB79410
AAY49914
AAX49915
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AAY99387
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                              (SLDH; AAB22172) and to the gene encoding it (AAA97430). SLDH has a molecular weight of about 54 kDa and catalyses the conversion of D-sorbitol into L-sorbose using NADP+ as a co-enzyme. SLDH specifically catalyses the oxidation of sorbitol, mannitol and arabitol, but does not act on xylitol, ribitol, inositol and glycerol. The invention also encompasses expression vectors and host cells comprising the Gluconobacter oxydans SLDH gene, and the recombinant production of SLDH. The invention further relates to a method for preparing L-sorbose by contacting the recombinant SLDH with D-sorbitol; a process for producing 2.* keto-L-gluconic acid by contacting recombinantly produced sorbose
                                                                                                                                                                                                                                                                                                      dehydrogenase and/or sorbosone dehydrogenase with L-sorbose; and a process for preparing L-ascorbic acid or its alkaline earth metals salts by conversion from 2-keto-L-gluconic acid. SLDH is useful for producing L-sorbose or 2-keto-L-gluconic acid as an intermediate in L-ascorbic
                                                                                                                   The invention relates to Gluconobacter oxydans D-sorbitol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLTGSDRSKKKAEEFKAQDCLYSLTETAPSGKSTVRVMGALRDYLLAPADPEAVLKHLVD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gluconobacter oxydans derived D-sorbitol dehydrogenase obtainable by
               culturing its gene-transformed host cells, useful for producing
L-sorbose or 2-keto-L-gluconic acid as an intermediate in L-ascorbic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MITRETLKSLPANVQAPPYDIDGIKPGIVHFGVGNFFRAHEAFYVEQILEHAPDWAIVGV 60
                                                                                                                                                                                                                                                                                                                                                                          production. The present sequence represents the Gluconobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKLNAASGLDDDLPLVAEDFHOWVLEDOFADGRPPLEKAGVOMVGDVTDWEYVKIRMLNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSNKAMSDQTLRIASDGCSKVQVFWTETVRRAIEDKRDLSRIAFGIASYLEMLRGRDEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 485;
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0
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Pred. No. 0;
; Mismatches
                                                                                5; Page 58-60; 72pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
100.0%;
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Best Local Similarity 100.
Matches 485; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          oxydans SLDH protein.
                                                                                                                                                                                                                                                                                                                                                                                                                          485 AA;
                                                 production
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                                                                                  Claim
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                                                  acid
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AAY49913 standard; Protein; 485 AA.

AAY49913

AAY49913;

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Set of genetically modified mutants not containing L sorbose reductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                nullified by gene recombination gene. The present sequence represents Gluconobacter suboxydans L-sorbose reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gluconobacter suboxydans L-sorbose reductase.
                                                              3luconobacter suboxydans; L-sorbose reductase; genetic engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                     Gluconobacter suboxydans L-sorbose reductase protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 MSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSA 237
                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a genetically engineered microorganism derived from a microorganism belonging to the Gluconobacter or Acetobacter which is characterised in that
                                                                                                                                                                                                                                                                                                                                                                                                                           biological activity for reducing L-sorbose is substantially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 MSCDNLRHNGNVARKAFLGYAKARDPELAKWIEENATFPNGMVDRITPTVSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.6e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.7%; Score 52; DB Best Local Similarity 100.0%; Pred. No. 3.6 Matches 52; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 18-21; 33pp; English..
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99JP-0224679.
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                                                                                                      Gluconobacter suboxydans
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                                                                                                                                                                                                                                                                                          WPI; 1999-579276/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           485 AA;
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06-AUG-1999;
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                                                                             mutant.
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N-PSDB; AAH65091
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08-JUL-1999;
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AAB79410
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                                                                                                                                                                                                                                                                   contacting the recombinant SLDH with D-sorbitol; a process for producing 2.keto-L-gluconic acid by contacting recombinantly produced sorbose dehydrogenase and/or sorbosone dehydrogenase with L-sorbose; and a process for preparing L-ascorbic acid or its alkaline earth metals salts by conversion from 2-keto-L- gluconic acid. SLDH is useful for producing L-sorbose or 2-keto-L- gluconic acid. SLDH is useful for producing acid production. The present sequence represents the N-terminal sequence of the Gluconobacter oxydans SLDH protein obtained in an exemplification.
                                                                                                                                                             The invention relates to Gluconobacter oxydans D-sorbitol dehydrogenase (SLDH: AAB21172) and to the gene encoding it (AAA97430). SLDH has a molecular weight of about 54 kba and catalyses the conversion of D-sorbitol into L-sorbose using NADP+ as a co-enzyme. SLDH specifically catalyses the oxidation of sorbitol, mannitol and arabitol, but does not act on xylitol, ribitol, inositol and glycerol. The invention also encompasses expression vectors and host cells comprising the Gluconobacter oxydans SLDH gene, and the recombinant production of SLDH. The invention further relates to a method for preparing L-sorbose by
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                               Gluconobacter oxydans derived D-sorbitol dehydrogenase obtainable by culturing its gene-transformed host cells, useful for producing L-sorbose or 2-keto-L-gluconic acid as an intermediate in L-ascorbic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 10; DB 21; Length 10; 100.0%; Pred. No. 0.015; 1ve 0; Mismatches 0; Indels
                          Saito Y;
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                          Noguchi Y,
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Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glutamicum protein fragment SEQ ID NO: 3626.
                          Matsuura M,
                                                                                                                                       Example 2; Page 28; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG89872 standard; Protein; 503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizoguchi H, Ando S,
Senoh A, Ikeda M, O
(FUJI ) FUJISAWA PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-0377484.
2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
                        Ichikawa C,
, Takata Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organic acid synthesis.
                                                           WPI; 2000-587530/55
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MITRETLKSL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA;
                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                    acid production
                                    Yamashita M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2001
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Tateishi N,
                        Shibata T,
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG89872;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                          The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a
                                                                                                                                                                                                                                                                                                                                                                                                                    mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; monproteinogenic acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                               Claim 17; SEQ ID NO: 3626; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; Corynebacterium diphtheriae; evolutionary study
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.9%; Score 9; DB 2
100.0%; Pred. No. 4.5
ive 0; Mismatches
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100.0%; Pre-
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99DE-1031433.
99DE-1031434.
99DE-1031510.
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99DE-1031420.
99DE-1031424.
99DE-1031428.
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99DE-1031413.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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2001-376931/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 PGIVHFGVG 34
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WPI; 1999-579276/49.
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                                                                                                                                                                                                                                                                                             13-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primers.
                                                                                                                                             AU9920390-A
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                                                                                                                                                                                                                                                                                                                                                                                          Hoshino T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                  mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY49915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAPT1360 to AAF71750 encode the Corynebacterium glutamicum sugar metabolism and oxidative phosphorylation (SMP) proteins given in AABF9243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleoside, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corynebacterium diphtheriae in a subject. (I), (II), (III) or bost cells containing them are used to map genomes of organisms related to corynebacterium identify and localise C. glutamicum, sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the containing the metabolism of sugars, and in modulating high-energy molecule production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gluconobacter suboxydans L-sorbose reductase peptide SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haberhauer G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.9%; Score 9; DB 2
100.0%; Pred. No. 4.5
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schroeder H,
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99US-0151572.
99DE-1042076.
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                                                                                             99DE-1032230
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99DE-1042125
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carbohydrates or enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pompejus M, Kroeger B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-061975/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 PGIVHFGVG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGIVHFGVG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF71527
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03-SEP-19
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AAY49914
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Set of genetically modified mutants not containing L sorbose reductase
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Gluconobacter suboxydans; L-sorbose reductase; genetic engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gluconobacter suboxydans; L-sorbose reductase; genetic engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gluconobacter suboxydans L-sorbose reductase peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biological activity for reducing L-sorbose is substantially
nullified by gene recombination. The present sequence represents
a Gluconobacter suboxydans L-sorbose reductase peptide, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an example from the present invention for generating degenerate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a genetically engineered microorganism derived from a microorganism belonging to the Gluconobacter or Acetobacter which is characterised in that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6%; Score 8; DB 2
100.0%; Pred. No. 7.8
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                      Kon T;
                                                                                                                                                                                                                                                                                                                                                             (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                    Shinjoh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shinjoh M,
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                                                                                                                                                                                                                                                                                                       98EP-0104546.
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                                                                                Gluconobacter suboxydans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    Tazoe M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-579276/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AA;
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Homo sapiens.
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02-SEP-1998;
02-SEP-1998;
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01-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; hamatopolesis regulation; tissue growth; angiogenesis; activin; inhibin; chemoclactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; wasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; eardiatherosclerotic; antidiabetic; cytostatic; nootropic; cardiatis, antistyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
          Set of genetically modified mutants not containing L sorbose reductase
                                                                                                                                             PCR primers.
N.B. This patent is equivalent to the basic NO9901197 in week 199949.
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                   microorganism derived from a microorganism belonging to the genus Gluconobacter or Acetobacter which is characterised in that the biological activity for reducing L. sorbose is substantially nullified by gene recombination. The present sequence represents a Gluconobacter suboxydans L.sorbose reductase peptide, used in
                                                                                                                                   an example from the present invention for generating degenerate
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                                                                                                                                                                                                           1.6%; Score 8; DB 20; Length 8; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                                          The present invention describes a genetically engineered
                                                                                                                                                                                                                                                                                                                                                                                                                        Human reductase-like ORF2512 protein, SEQ ID NO:5024.
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                                                                                                                                                                                                                                                                                                                                                 ABP33539 standard; Protein; 103 AA.
                                 Example 3; Fig 2; 33pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                         Query Match 1.6
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leach MD, Shimkets RA;
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N-PSDB; ABN77565.
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polypeptices at least 00% indeficient to the ORFF protective to as ORFX) proteins, polynecledess at least 85% identical to referred to as ORFX) proteins, polynecledess at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polyneclectides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynecledides are thought of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide cange of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopolesis regulation, tissue growth, anglogenesis, activity, thrombolytic activity, chemotactic/ Chemokinetic activity, haemostatic activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, thrombolytic activity, and antiinflammatory activity, thrombolytic activity, and antiinflective activity, and behaviour. ORFX proteins, of bodily characteristics, fertility and behaviour. ORFX proteins, other proliferative disorders such as psoriasis and benign tumours, other proliferative disorders such as psoriasis and benign tumours, and any disorders such as psoriasis and benign tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, disorders of tissue growth and regeneration, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. OREX incleic acids may also be used as a source of primers and probes, in the detection of OREX genomic sequences or transcripts, in the identification and cloning of homologus sequences, in genetic diagnosis, and in forensic biology. The OREX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of OREX protein, and in drug screening. The OREX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of OREX-associated diseases.
                                      designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent CDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
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Sequences ABP31028-ABP35561 represent 4534 novel human proteins
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98US-0098821.
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980S-0099536.
980S-0099596.
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98US-0099792.
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98US-0099812.
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980S-0100684.
980S-0100711.
980S-0100919.
980S-0100930.
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98US-0102331.
98US-0102484.
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98US-0102570.
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98US-0099816.
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98US-0100662.
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20-OCT-1998;
20-OCT-1998;
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98US-0105002

98US-0105164

98US-0105166

98US-0105563

98US-0105694

98US-0105691

98US-0105691

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98US-0106023

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98US-0106032

98US-0106919

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98US-0108801

98US-0108849

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(GETH.) GENENTECH INC

Smith V, Watanabe CK, Wood WI; Gurney AL, Baker K, Goddard A,

WPI; 2000-237871/20. N-PSDB; AAA37069.

New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions

Claim 12; Fig 96; 773pp; English.

The AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.

163 AA; Sequence

; 1.6%; Score 8; DB 21; Length 163; 100.0%; Pred. No. 17; ive 0; Mismatches 0; Indels Query Match 1.6 Best Local Similarity 100. Matches 8; Conservative

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Gaps

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ANDLIATE ANDLATATOR TREPERCENT HOVEL HUMBER SECTEDLY AND CLARACTE ANDLATE ANDLATATOR AND CONTROL AND C
represent novel human secretory and transmembrane
The PRO polypeptides are useful to detect other
to link bicactive molecules to cells expressing
to modulate biological activities of cells expressing
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Pred. No. 17;
0; Mismatches
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99US-0162506.
99WO-US28313.
99WO-US28551.
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99US-0145698,
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2000WO-US00219.
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Pan J, Paoni NF, Roy MA,
Watanabe CK, Williams PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 LYSLTETA 88
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                                                                                                                                                                                                                                                                                                                      Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate, cervical; tumour necrosis factor-alpha; TNF-alpha; cartillage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                           AAU12423 standard; Protein; 163 AA.
                                                                                                                                                                                                                                                                                  Human PRO1273 polypeptide sequence.
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10-NOV-2000; 2000WO-US30873
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                                                                                                                                                                                                                                      24-OCT-2001 (first entry)
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N-PSDB; AAS21495.
                                       81 LYSLTETA 88
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06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
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24-FEB-2000;
24-FEB-2000;
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02-DEC-1999
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Length 163;

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Hillan KJ;
Gaps
                                                                                                                                                                                                                                                                                                          Secreted and transmembrane proteins and nucleic acids designated PRO,
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Gurney AL, H
A, Tumas D;
0; Indels
                                                                                                                                                                                                                                                             P. Botstein D, Desnoyers L, Eaton DL, F
Goddard A, Godowski PJ, Grimaldi CJ, Gu
Paoni NF, Roy MA, Smith V, Stewart TA,
                                                                                                                                                                                                                                                            Eaton DL,
                                                                                                           Secreted; transmembrane; gene therapy.
                                                                                                                                                                                                                                                                                Wood WI;
                                                        AAB66136 standard; protein; 163 AA
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Local Similarity
es 8; Conserv
             163 AA
                                                                                                 136 LYSLTETA 143
                                                                                  LYSLTETA 88
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                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                           ABB95524;
             Sequence
                                  Query Match
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                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC90701 to AAC90715 encode the human secretory proteins given in AAB3661 to AAB36675. The proteins can have cytostatic, anti-inflammatory, heamatopoietic, anti-iocagulant, immunomodulatory and hepatotropic activities, and can be used as cell migratory agents, cell proliferation stimulants and call differentiation inducers. The proteins are useful in the treatment and prevention of diseases such as cancer, lung function disorder, liver function disorder, agastrointestinal disorder and immune diseases. AAC90716 to AAC90755 represent PCR primers which are used in the exemplification of the present invention.
  gene mapping and gene
                                                                               probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents.

The nucleic acids may also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                          Human; secretory protein; cancer; immune disease; infectious disease; lung function disorder; liver function disorder; antinflammatory; gastrointestinal disorder; cytostatic; hematopoietic; anticoagulant; immunomodulatory; hepatotropic; cell proliferation-stimulant; cell migratory agent; cell differentiation-inducer.
                                                                     These proteins and the DNA encoding them may be used as hybridization
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel secretory protein and its salt with e.g. anti-cancer, anti-inflammatory and hematopoietic, effects, applicable as drugs in remedies and preventives to treat diseases like cancer and immune
                                                          The present invention relates to secreted and transmembrane proteins
                                                                                                                                                                                                       ó;
                                                                                                                                                                              1.6%; Score 8; DB 22; Length 163; 100.0%; Pred. No. 17;
                                                                                                                                                                                                     .0; Indels
useful as hybridization probes, in chromosome and
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                                                                                                                                                                                                                                                                                                                                                                                   Human secretory protein TGC-715 SEQ ID NO:11.
                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanaka H, Ohkubo
                                                                                                                                                                                                                                                                                                             AAB36671 standard; Protein; 163 AA
                                Claim 1; Fig 96; 787pp; English.
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                                                                                                                                                                                                       8; Conservative
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                                                                                                                                                                                           Local Similarity
                                                                                                                                                        163 AA;
                                                                                                                                                                                                                                           11111111
136 LYSLTETA 143
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                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                      AAB36671;
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             therapy
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Matches
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                                                   Gaps
                                                 .;
0
            Length 163;
                                                                                                                                                                                                                                                                                                                                                    Human angiogenesis related protein PRO1273 SEQ ID NO: 204.
                                                   Indels
                                                 Mismatches
            Score 8; I
Pred. No.
                                                                                                                                                                                                                                  ABB95524 standard; Protein; 163 AA.
1.6%; Scc.
100.0%; Pre
0; '
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2000US-0643657.
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                                                   Conservative
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03-JAN-2002
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                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tunmour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
                                                                                                                                                                                       Paoni NF;
                                                                                                                                                                                                                                                One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                  PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, FF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                           Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%; Score 8; DB 23; Length 163; 100.0%; Pred. No. 17; 0; Mismatches 0; Indels
                                                                                                                                                                            Gerber H, Gerritsen ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                healing; chromosome mapping; gene mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO1273 protein sequence SEQ ID NO:204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB84918 standard; Protein; 163 AA
                                                                                                                                                                                                                                                                                        Claim 11; Fig 204; 567pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0% Matches 8; Conservative
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                                       GERRITSEN M E.
                                                                      GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                           Ferrara N,
                                                            GODOWSKI P J.
                                                                                                                                 WATANABE C K.
WILLIAMS P M.
                                                                                                            PAONI N F.
STEPHAN J F.
                                                                                                                                                                                                                  WPI; 2002-171999/22.
N-PSDB; ABL95662.
                   FERRARA N.
                                                  GODDARD A.
                                                                                                                                                                                                                                                                                                                                                                                                       163 AA;
                                                                                                                       (STEP/) STEPHAN J
(WATA/) WATANABE C
(WILL/) WILLIAMS P
(WOOD/) WOOD W I.
                              GERBER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 LYSLTETA 143
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                                                                                                    PAN J.
PAONI I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200200690-A2
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                                                (GODD/)
(GODO/)
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(MARS/)
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(PAON/)
                   FERR/)
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ABB84918
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ABBBS003. The PRO proceins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver acarcinoma and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
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Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
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Godowski PJ, Gurney AL, Hillan KJ, Marsters SA,
Stephan JF, Watanabe CK, Williams PM, Wood WI,
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2000US-220664P
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28-FEB-2001;
25-JUL-2000;
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08-NOV-2000;
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Length 163;

DB 23;

1.6%; Score 8;

Query Match

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Gaps

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Length 163; 0; Indels

Score 8; DB 23; Pred. No. 17; 0; Mismatches

1.6%; Scor. 100.0%; Pred 0; N

163 AA;

8, 2003, 16:42:50

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cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating or inhibiting the proliferation of normal human blood, for stimulating or inhibiting the proliferation of normal human blood, for stimulating or inhibiting the proliferation of normal human blood, for brobbast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have and in chromosome and gene mapping. Adu83592-Adu83713 represent human PRO protein sequences of the invention.
                                                                                                                                                                                                                                               Query Match 1.6
Best Local Similarity 100.
Matches 8; Conservative
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Job time : 57 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polypucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                  Gaps
                                                                                                                                                                                                                                                                                                               Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha
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               Pred. No. 17;
                                Mismatches
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                                                                                                                                                                               AAU83683 standard; Protein; 163 AA
                                                                                                                                                                                                                                                                                Human PRO protein, Seq ID No 184.
100.08; Pr.
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Grimaldi JC, Gurney AL,
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N-PSDB; ABK33627.
             Best Local Similarity
Matches 8; Conserv
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TITLE OF INVENTION:
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993
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Maximum DB seq length: 200000000
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Sequence 5, Appli Sequence 25, Appli Sequence 25, Appl Sequence 25, Appl Sequence 29, Appl Sequence 29, Appl Sequence 11, Appli Sequence 11, Appli	Sequence 34, Appl Sequence 6, Appli Sequence 73, Appl
US-08-448-250-5 US-08-426-236-2 US-08-655-259-25 US-08-762-500-25 US-08-286-819A-29 US-09-144-085-1 US-09-144-085-1 US-08-159-339A-1157 US-08-159-339A-1157 US-08-236-385A-11 US-08-236-385A-11 US-08-236-385A-11 US-08-31-071A-19 US-08-321-071A-19 US-08-321-071A-19	US-08-041-155D-54 US-08-942-686-6 US-07-998-003A-73
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## ALIGNMENTS

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18.507-96.187-4
Sequence 4.87-4701
Sequence 4.87-701
Sequence 6.87-701
Sequence 6.87-701
Sequence 7.85.5. Catherine
APPLICANT: SAS.5. Catherine
APPLICANT: SAS.5. Catherine
APPLICANT: SAS.5. Catherine
APPLICANT: SAS.5. Catherine
APPLICANT: COPRANTION: Proceed in Aving beta 1.3 glucanase activity, bacteria
TITLE OF INVENTION: Containing this DNA, transformed plant cells and plants:
TITLE OF INVENTION: Containing this DNA, transformed plant cells and plants:
CORRESPONDENCE ADDRESS: 26
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CONTRIT. ALEXANDEIA
STATE: ATRAINE ADDRESS: 29
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIAL BLOOM
STATE: TBM PC COMPATIAL BLOOM
STATE: URB PC COMPATIAL BLOOM
STATE: 1930125
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Indels

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Sequence 5, Application US/07927391
Patent No. 6001649
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FERRARA, Pascual
APPLICANT: MILOUX, Brigitte
APPLICANT: MINTY, Adrian
APPLICANT: MINTY, Adrian
APPLICANT: WINTY, Adaian
APPLICANT: WINTY, Natalio
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: for its preparation.
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS::
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APPLICANT: Plutzky, Jorge
APPLICANT: Neel, Benjamin G.
APPLICANT: Rosenberg, Robert D.
TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/927,391 FILING DATE: 19920929 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 3; Pred. No. 9.8; 0; Mismatches
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFO 53
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08202389
Patent No. 5536636
GENERAL INFORMATION:
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 683-410
TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-07-927-391-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Best Local Similarity
Matches 7; Conserv
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ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 APSGKST 94
                                       88 APSGKST 94
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                                                               APSGKST
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US-08-202-389-10
   7;
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   Matches
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TITLE OF INVENTION: Protein having a cytokine type
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
TITLE OF INVENTION: transformed cells and microorganisms.
                                                                            Gaps
                                                                            ;
0
                                     Length 25;
                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARACHIEN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
. 9.8;
                                       DB 1;
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KAGHAD, Mourad
LABIT-LE BOUTEILLER, Christine
                                                                          Mismatches
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100.0%; Pred. No.
                                         Score 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16781/383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FF 91 03904
FILING DATE: 29-WAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                     CAPUT, Daniel
FERRARA, Pascual
GUILLEMOT, Jean-Claude
LEPLATOIS, Pascal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: FR 91 00137
FTI.ING DATE: 08-JAN-1992
                       1.4%; Sco.
100.0%; Pre
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; Sequence 3, Application US/08371121
; Patent No. 5652123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
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TELEAX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
ELENTH: 25 amino acids
"VPE: amino acid
"inear"
                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: FOLEY
STREET: 3000 K St
CITY: Washington,
COUNTRY: USA
ZIP: 20007-5109
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Best Local Similarity
                                     Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                88 APSGKST 94
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2 APSGKST 8
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APPLICANT:
APPLICANT:
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APPLICANT:
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US-07-966-187-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows 95
SOFTWARE: FastESQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7; DB 2;
Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                    CSHL96-03
                                  US/08/685,992
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; Patent No. 5951979
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION UNDRER:
FILING DATE: July 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION:
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Best Local Similarity 100.0%;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                 25-JUL-1996
                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Mil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02421-4799
                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 IIREKGV 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 IIREKGV 221
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                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,389
FILING DAMPE: 28-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08685992
Sequence 12, Application US/08685992
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,926
FILING DATE: 01-DEC-1992
PRIOR APPLICATION NUMBER: US 07/829,141
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/721,112
FILING DATE: 26-UON-1991
ATTORNIC DATE: 26-UON-1991
ATTORNIC DATE: A-GARDIAN: PATFICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE, DOCKET NUMBER: B1H92-05MA
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4%; Score 7;
100.0%; Pred. N
Live 0; Misma
                                                                  ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
CITY: Lexington
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amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-202-389-10
                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                             CITY: Lexi
STATE: MA
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STATE: MA
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266 amino acids

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Gaps

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APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COUVALIN PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESSE:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ATREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                       Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/980,357 CIRCLENG DATE:
                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-AGG-1994
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AGG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FK/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
ATTORNY AGENT INFORMATION:
NAME: Oblon, NO. 6013508man F.
BREISTRATION NUMBER: 24.618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                            1.4%; Score 7; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/08980357
Patent No. 6013508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MC SOFTWARE: PATOT
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(703) 413-2220
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                              Best Local Similarity 100.
Matches 7; Conservative
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-819A-23
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                              215 KWIEENA 221
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185 KWIEENA 191
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                                                                                                                                                                                                                                                                                                                      RESULT 8
US-08-980-357-23
                                                                                                 Query Match
                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
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                                                                                                                                                      Length 266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/286,819A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                   1.4%; Score 7; DB 2
100.0%; Pred. No. 81;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-ACT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
FLECCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
THE COMMUNICATION INFORMATION:
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THE COMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08286819A Patent No. 5871910 GENERAL INFORMATION: APPLICANT: ARTHUR, MICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DUKTA-MALEN, SYLVIE
MOLINAS, CATHERINE
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
                                                                                                                                                      Query Match 1.4
Best Local Similarity 100.
Matches 7; Conservative
                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-144-925-12
            amino acid
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215 IIREKGV 221
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US-08-286-819A-23
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Length 366;
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TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
                                                                                                           ourTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 3; L4
Pred. No. 1.1e+02
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REFERENCE/DOCKET NUMBER: FD2279 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/153,733A
                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09153733A Patent No. 6025475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/481,377
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDY, A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
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TELEPHONE: 301-309-8504
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TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 366 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                              TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100...
7: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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STATE: CALIFORNIA
    MARYLAND
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APPLICANT: JOHNS
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US-09-153-733A-6
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                      COUNTRY:
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                    Length 303;
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                                                        0; Indels
                                                                                                                                                                                                                                                                                     APPLICANT: JOHNS HOPKINS UNIVERSITY TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3 NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,377
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANCELES
CATTE: CALIFORNIA
COUNTRY: US
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APPLICANT: SOPPET, DANIEL
TITLE OF INVENTION: GROWTH FACTOR HTTER36
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: WETHERELL, JR. Ph.D., JOHN R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD2279 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00666
FILING DATE: 12-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
    1.4%; Sco.
100.0%; Pre
0;
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Patent No. 6004780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 366 amino acids
Query Match
Best Local Similarity 100.0
Local 7; Conservative
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Matches 7; Conservative
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; MOLECULE TYPE: protein
US-08-481-377-6
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185 KWIEENA 191
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                                                                                           215 KWIEENA 221
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51 VLRKIIR 57
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Gaps

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TITLE OF INVENTION: GROWTH FACTOR HTTER36
                  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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| 51 VLRKIIR 57
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TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                        DB 3; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
REGISTRATION NUMBER: 31.678
REFERENCE/DOCKET NUMBER: FD2279 PCT
                                                                                           1.4%; Stor.
100.0%; Pred. No. _
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/389,705
FILING DATE: 03-Sep-1999
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/153,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Best Local Similarity 100.0%; Pred. No.
Matches 7; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-389-705-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09389705
Patent No. 6391565
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-357-905-9; Sequence 9, Application US/09357905; Patent No. 6413933; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 366 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SOPPET, DANIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90067
COMPUTER READABLE FORM:
: 366 amino acids
amino acid
                                                                                      Query Match
Best Local Similarity 100..
                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-153-733A-6
                                                                                                                                                                            469 VLRKIIR 475
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51 VLRKIIR 57
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US-09-389-705-6
LENGTH:
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                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application PC/TUS9400666
GENERAL INFORMATION:
APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPULES: 1244 CONFESSION #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00666
FILING DATE: 12-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; DB 4; Le
Pred. No. 1.1e+02;
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STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
COUTTE: CALIFORNIA
COUNTRY: US
ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,905
FILING DATE: 21-Jul-1999
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION DATE:
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-09-357-905-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDY, A.
REGISTRATION NUMBER: 373
REFERENCE/DOCKET NUMBER: PFZ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 366 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 1.4%; Scr
Best Local Similarity 100.0%; P.
Matches 7; Conservative 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEFAX: 301-309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                      ZIP: 20850 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                        STATE: MARYLAND
                                                     CITY: ROCKVILLE
                                                                                                   COUNTRY: USA
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APPLICANT: Rahng, Lyn Sue
APPLICANT: Bapiro, Lucy
APPLICANT: Bankovic, Stephen J
APPLICANT: Berkovic, Stephen J
APPLICANT: Berkovic, Stephen J
APPLICANT: Berdis, Anthony
APPLICANT: Berdis, Anthony
APPLICANT: Berdis, Anthony
APPLICANT: Bergis, Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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1.4%; Score 7; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
REFERENCE/DOCKET NUMBER: FD2279 PCT TELECOMMUNICATION INFORMATION: TTELEPHONE: (619) 455-5100
TTELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acids
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Job time : 40 secs
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US-09-269-137-4
Sequence 4, Application US/09269137
Patent No. 6413751
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Inear
MOLECULE TYPE: protein
PCT-US94-00666-6
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364 LRKIIRE 370
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZGUCHI, HIROSHI
APPLICANT: HAYASHI, MIKIRO
APPLICANT: HOSHI, MIKIRO
APPLICANT: TATELSHI, NACKO
APPLICANT: TATELSHI, NACKO
APPLICANT: TATELSHI, NACKO
APPLICANT: TATELSHI, NACKO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPREMENE: 249-125
CURRENT FILING DATE: 2000-12-16
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
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100.0%; Pred. No. 2.2
ive 0; Mismatches
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100.08; Li
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SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3626
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  Best Local Similarity
Matches 9; Conserv
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US-10-142-419-504
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Copyright (c) 1993 - 2003
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                                                        protein search, using sw model
                                                                                                                                                                        OLIGO Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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485
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Match Length
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Gaps

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Length 503; Indels

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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR APPLICATION NUMBER: 60/063327
PRIOR APPLICATION NUMBER: 60/063327
PRIOR APPLICATION NUMBER: 60/063329
                              Sequence 504, Application US/10028072 Publication No. US20030004311A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60/063561
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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                                                                                                                                                             Beresini,Maureen
DeForge,Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumas, Daniel
Watanabe, Colin K
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                                                                                                                                                                                                                                                                                                                                                                                          Godowski, Paul
Gurney, Austin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                            Goddard, Audrey
                                                                                                                               APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLICANT: Zhang
TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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-10-028-072-504
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PRIOR PELICATION NUMBER: 60/065846
PRIOR PELICATION NUMBER: 60/065846
PRIOR PELING DATE: 1997-11-12
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081818
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PRIOR FILING DATE: 1986-04-14
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC54
CURRENT APPLICATION NUMBER: U5/10/123,904
                                                                                                                                                                                               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RL017
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NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/121,049 CURRENT FILING DATE: 2002-04-12
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                                                                                                                         Stewart, Timothy A
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Stewart, Timothy A
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                 Gerritsen, Mary E
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Wood, William
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DeForge, Laura
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Wood, William
                                                                                       Sherwood, Steven
Smith, Victoria
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Filvaroff, Ellen
                                                   Godowski, Paul J
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                                                                      Gurney, Austin L
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Gao, Wei-Qiang
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US-10-123-904-504
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US-10-121-049-504
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Best Local Similarity
Matches 8; Conserv
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LENGTH: 163
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LENGTH: 163
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Pred. No.
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Publication No. US20030022239Al
GENERAL INFORMATION:
APPLICANT: Baker.Kevin P.
APPLICANT: Beresini, Maureen
                                           APPLICATION NUMBER: 60/085338
FILING DATE: 1998-05-13
                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/086430 FILING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                   ICATION NUMBER: 60/087106
NG DATE: 1998-05-28
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-23
                                                                                   LICATION NUMBER: 60/085339
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LING DATE: 1998-05-15
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FILING DATE: 1998-05-15
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-26
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PRIOR FILING DATE: 1998-07-07
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RL0382
CURRENT APPLICATION NUMBER: U5/10/176,918
CURRENT APPLICATION NUMBER: U5/10/176,918
PRIOR APPLICATION NUMBER: S002-06-20
PRIOR APPLICATION FEMOWED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
               TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                        TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C353 CURRENT APPLICATION NUMBER: US/10/175,746 CURRENT FILING DATE: 2002-06-19 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
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Mismatches
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; Sequence 504, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
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Filvaroff, Ellen
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Best Local Similarity 100.
Matches 8; Conservative
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; ORGANISM: Homo Sapien
US-10-176-918-504
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; ORGANISM: Homo Sapien
US-10-175-746-504
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Best Local Similarity
Matches 8; Conserv
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LENGTH: 163
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33330R1C160
                   Gaps
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CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 504
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 Pred. No. 7.9;
               Mismatches
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100.0%;
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Wood, William
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Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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Filvaroff, Ellen
Gao, Wei-Qiang
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Best Local Similarity 100.
Matches 8; Conservative
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                 8; Conservative
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; ORGANISM: Homo Sapien
US-10-140-470-504
Best Local Similarity
                                                                   136 LYSLTETA 143
                                                 81 LYSLTETA 88
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                                                                                                                                                                                    Publication No.
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R FILING DATE: 1998-07-0/
IR APPLICATION NUMBER: 60/095302
JR FILING DATE: 1998-08-04
OR APPLICATION NUMBER: 60/095318
OR APPLICATION NUMBER: 60/095318
                              R FILING DATE: 1998-03-26
R RAPLICATION UNMBER: 60/079728
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/081819
R RPLING DATE: 1998-04-15
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PRIOR PILING DATE: 1998-09-10
PRIOR PAPLICATION NUMBER: 60/100038
PRIOR PILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR APPLICATION NUMBER: 60/100385
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FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100848
FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/100919
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APPLICATION NUMBER: 60/085579
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FILING DATE: 1998-05-22
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/091982
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FILING DATE: 1998-08-10
APPLICATION NUMBER: 60/096146
FILING DATE: 1998-08-11
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FILING DATE: 1998-09-09
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099811
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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
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FILING DATE: 1998-04-22
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FILING DATE: 1998-05-06
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FILING DATE: 1998-05-13
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/097986
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APPLICATION NUMBER: 60/098544
FILING DATE: 1998-08-31
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/096791
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APPLICATION NUMBER: 60/099812
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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P530PLC79
CURRENT APPLICATION NUMBER: U5/10/227,884
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: U6/10/9,480
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06213
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330VICE: P3340VICE: US/10/176,921
CURRENT APPLICATION NUMBER: US/10/176,921
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
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Publication No. US20030027988A1
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FILING DATE: 1998-03-20
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Best Local Similarity 100.0%;
Matches 8; Conservative 0
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Wood, William
                                                                                                      Gerritsen, Mary E
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                                                                                                                                                                              Godowski, Paul J
Gurney, Austin L
                                                                                                                                                                                                                                                     Sherwood, Steven
                                                                                                                                                                                                                                                                                        Smith, Victoria
                                                                       Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                            Tumas,Daniel
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; ORGANISM: Homo Sapien
US-10-176-921-504
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R APPLICATION NUMBER: 60/101477

R FILING DATE: 1998-09-23

RR FILING DATE: 1998-09-24

RR FILING DATE: 1998-09-24

RR APPLICATION NUMBER: 60/101741

RR FILING DATE: 1998-09-24

RR FILING DATE: 1998-09-24

RR PELICATION NUMBER: 60/10196

RR FILING DATE: 1998-09-25

RR APPLICATION NUMBER: 60/101916

RR FILING DATE: 1998-09-24

RR FILING DATE: 1998-09-24
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FILING DATE: 1999-02-10
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FILING DATE: 1999-06-22
APPLICATION NUMBER: 60/140723
FILING DATE: 1999-06-22
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FILING DATE: 1998-10-28
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IG DATE: 1998-10-29
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FILING DATE: 1998-10-30
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NG DATE: 1998-11-03
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ING DATE: 1998-11-17
LICATION NUMBER: 60/108801
ING DATE: 1998-11-17
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NG DATE: 1998-11-18
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FILING DATE: 1998-12-15
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FILING DATE: 1998-12-22
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ILING DATE: 1998-12-23
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LCATION NUMBER: 60/115558
NG DATE: 1999-01-12
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NG DATE: 1999-01-12
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APPLICATION NUMBER: 60/130232
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FILING DATE: 1999-04-26
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APPLICATION NUMBER: 60/134287
FILING DATE: 1999-05-14
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FILING DATE: 1999-06-23
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FILING DATE: 1999-07-20
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330TLG54
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
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100.0%; Pred. No. 7.9;
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Pred. No. 7.9;
0; Mismatches
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0; Mismatches
               PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-06-03
PRIOR PELING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APLICATION NUMBER: 60/164418
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o. US20030032155A1
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PRIOR APPLICATION UNDBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
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PRIOR APPLICATION NUMBER: 60/169445
FILING DATE: 1999-07-28 APPLICATION NUMBER: 60/146963
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PRIOR APPLICATION NUMBER: 60/166361
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Watanabe, Colin K
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Filvaroff, Ellen
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Sherwood, Steven
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Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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| 136 LYSLTETA 143
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Publication No. US20
GENERAL INFORMATION
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Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 504
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                    ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-431-504
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; ORGANISM: Homo Sapien
US-10-143-114-504
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|136 LYSLTETA 143
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CURRENT APPLICATION NUMBER: US/10/140,474.
CURRENT FILING DATE: 2002-05-06
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R10251
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                                                                Sequence 504, Application US/10140474
Publication No. US20030032156Al
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APPLICANT: Beresini, Maureen
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Wood, William
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Filvaroff, Ellen
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Gurney, Austin L.
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Filvaroff, Ellen
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C211
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             Length 163;
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CURRENT FILING DATE: 2002-05-09
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
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                                                Mismatches
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             Score 8;
Pred. No.
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Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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1.6%; SLL-
100.0%; Pre
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Best Local Similarity 100.0%; P:
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Wood, William
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Filvaroff, Ellen
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APPLICATION NUMBER: 60/113296
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FILING DATE: 1999-01-12
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FILING DATE: 1999-01-12
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ILING DATE: 1998-09-15
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NG DATE: 1998-09-18
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ILLING DATE: 1998-09-24
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                                                         ILING DATE: 1998-09-10
PPLICATION NUMBER: 60/099811
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ATE: 1998-11-18
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ILING DATE: 1998-09-23
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                                                PRIOR
   PPLICANT: Stephan, Jean-Philippe F.

APLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ITLE OF INVENTION: ACIDS ENCODING THE SAME

ILE REFERENCE: P3530P1C96
                                                                                CURRENT APPLICATION NUMBER: US/10/230,163
CURRENT FILING DATE: 2002-08-28
THEN APPLICATION NUMBER: 10/119,480
PRICE FILING DATE: 2002-04-09
PRICE APPLICATION NUMBER: 60/059113
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APPLICATION NUMBER: 60/095318
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P330RITON: ACIDS ENCODING THE SAME FILE REFERENCE: P330RITON: WINDER: US/10/140,002 CURRENT FILING DATE: 2002-05-06 Prior Application removed - See Palm or File Wrapper NUMBER OF SEO ID NOS: 550 SEO ID NOS: 550
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Watanabe, Colin K
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Best Local Similarity 100.
Matches 8; Conservative
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; ORGANISM: Homo Sapien
US-10-140-002-504
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Job time : 34 secs
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tive 0; Mismatches
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FILING DATE: 1999-04-27
APPLICATION NUMBER: 60/131291
FILING DATE: 1999-04-27
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FILING DATE: 1999-06-23
APPLICATION NUMBER: 60/144758
FILING DATE: 1999-07-20
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FILING DATE: 1999-07-26
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APPLICATION NUMBER: 60/131022
FILING DATE: 1999-04-26
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FILING DATE: 1999-04-28
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FILING DATE: 1999-08-03
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FILING DATE: 1999-08-17
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FILING DATE: 1999-08-31
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FILING DATE: 1999-12-07
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FILING DATE: 1999-05-14
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Tumas, Daniel
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Filvaroff, Ellen
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Matches 8; Conservative
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Smith, Victoria
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